

## TECHNICAL FIELD OF THE INVENTION

## BACKGROUND

The elongation cycle of protein synthesis is driven by two elongation factors that bind to nearly identical sites on the large (50S) ribosomal subunit (Spahn and Nierhaus, 1998; Wilson and Noller, 1998). EF-Tu delivers aminoacyl tRNAs to the ribosome, whereas EF-G catalyzes the translocation of the ribosome by one codon relative to the mRNA and the concomitant movement of the A and P site tRNAs. Both elongation factors are G proteins, and their interactions with the ribosome are coupled to the binding and hydrolysis of GTP. Like most G proteins, EF-Tu and EF-G are molecular switches that have limited inherent GTPase activity, and they rely on an accessory factor to stimulate activity at the appropriate time. This accessory factor is an integral part of the 50S ribosomal subunit and has usually been referred to as the “GTPase center,” but by analogy with the functionally equivalent GAP proteins that stimulate GTPase activity in G-proteins, it seems more appropriate to refer to it as the “GTPase activating region” (hereafter abbreviated as the GAR). Early work on the identification of the molecular components of the GAR implicated a complex between ribosomal protein L11 and a highly conserved 58-nucleotide stretch of 23S ribosomal RNA

(rRNA), nucleotides 1051-1108 in *Escherichia coli* (Schmidt et al., 1981; Thompson et al., 1979). The L11-RNA complex is the target for a family of thiazole antibiotics that includes thiostrepton and micrococcin. Thiostrepton binds essentially irreversibly to 50S subunits (Sopori and Lengyel, 1972) and inhibits hydrolysis of GTP by EF-G (Pestka, 1970; Rodnina et al., 1997), while micrococcin binds to the same complex and stimulates GTP hydrolysis by EF-G (Cundliffe and Thompson, 1981).

Other components of the ribosome have also been implicated in stimulation of GTP hydrolysis by elongation factors. Classical work suggested that protein L7/L12, which together with L10 forms the “stalk” of the 50S subunit that lies adjacent to L11, is involved in stimulation of GTPase activity in EF-Tu (Donner et al., 1978). However, recently it has been shown that protein L7/L12, although essential for stalk formation, is not required for viability in yeast (Briones et al., 1998). The sarcin/ricin loop, a small, highly conserved stem-loop in the 23S rRNA that is known to be essential for ribosome function, has been footprinted by the elongation factors (Moazed et al., 1988), and is also considered a candidate for being part of the GAR. Therefore, it is not yet clear whether the L11-RNA complex *per se* should be considered the GAR, or whether the GAR should be defined as a more extensive region of the 50S subunit. In any event, it appears that the L11-RNA complex is at the heart of the GAR; the complex of L11 with its cognate RNA will be referred to herein as the GAR.

The GAR is one of the most thoroughly characterized RNA-protein complexes. The secondary structure of the RNA was first inferred from biochemical and genetic studies (Glitz et al., 1981; Noller et al., 1981). It consists of a junction of four double-helical stems (Figure 1A). Approximately one-third of the residues in the GAR RNA are very highly conserved. The structure, thermodynamic stability, and ion-binding affinities of the RNA

component have been extensively probed by a variety of biophysical and biochemical techniques; these data suggest that the 1067 and 1095 stem-loops are folded into a compact tertiary structure (Conn et al., 1998; Rosendahl and Douthwaite, 1994). Protein L11 consists of two domains: the C-terminal domain binds tightly to the RNA tertiary structure, while the N-terminal domain is required for the cooperative interaction with thiostrepton (Xing and Draper, 1996). The structure of the C-terminal domain has been determined by NMR techniques (Hinck et al., 1997; Markus et al., 1997). Footprinting studies (Rosendahl and Douthwaite, 1993) have identified regions of RNA involved in the interaction with L11, while NMR chemical shift measurements (Hinck et al., 1997) have identified an RNA-binding surface on the C-terminal domain of the protein.

It is an object of the invention to provide a detailed view of a functionally important protein-RNA complex in the ribosome.

It is also an object of the invention to provide a high-resolution structure of a ribosomal protein-RNA complex.

Yet another object of the invention is to provide new principles of RNA folding, of RNA-protein recognition, and of indirect RNA tertiary structure stabilization.

Yet another object of the invention is to solve the three dimensional structure of L11 complexed with GAR RNA and to determine its structure coordinates.

## **SUMMARY OF THE INVENTION**

The present invention is broadly directed to methods of screening ribosomal protein L11/GTPase activating region (GAR) RNA-modulating compounds by using information from the high-resolution structure of the L11/GAR complex.

The invention encompasses use of the structure coordinates of an L11/GAR crystal to define the atomic details of regions of the L11/GAR complex, such as the GTPase activating region and one or more binding sites of accessory factors, which are target sites for inhibitors or activators.

The invention also encompasses use of the structure coordinates and atomic details of the L11/GAR RNA complex or its co-complexes to design, evaluate computationally, synthesize and use inhibitors or activators of the L11/GAR.

Structure coordinates for L11/GAR RNA complex according to Table II may be modified from this original set by mathematical manipulation. Such manipulations include, but are not limited to , crystallographic permutations, fractionalizations, or inversion of the raw structure coordinates, integer additions or subtractions to sets of the raw structure coordinates, and any combination of the above.

The crystal structure of the GAR allows the screening and design of novel classes of GAR inhibitory or activating compounds with great medical potential, for example, to prevent or stimulate growth of certain bacteria.

The invention encompasses a method for identifying a potential modulator of ribosomal protein L11/GAR activity, comprising the steps of: a) using a three-dimensional structure of the L11/GAR complex as defined by atomic coordinates of the L11/GAR according to FIG. 7; b) employing the three-dimensional structure to design or select the potential modulator; c) providing the potential modulator; and d) contacting the potential modulator with L11/GAR in the presence of an activity to determine the ability of the potential modulator to modulate the activity, for example, L11/GAR activity.

In one embodiment of the invention, the potential modulator is designed de novo.

In another embodiment of the invention, the potential modulator is designed from a

known modulator.

In another embodiment of the invention, the step of employing the three-dimensional structure to design or select the compound comprises the steps of: a) identifying chemical entities or fragments capable of associating with the L11/GAR; and b) assembling the identified chemical entities or fragments into a single molecule to provide the structure of the potential modulator. Relative to this embodiment, the potential modulator may be designed de novo or designed from a known modulator.

The invention further encompasses a method for screening L11/GAR-binding compounds comprising the steps of: 1) incubating in vitro one or more compounds, a known L11/GAR binding activity and labeled RNA comprising GAR RNA; 2) separating that fraction of the labeled RNA bound to the known L11/GAR binding activity from that fraction of the labeled RNA not bound to the known L11/GAR binding activity; and 3) detecting labeled RNA, wherein a decrease in the level of the labeled RNA bound to the known L11/GAR binding activity in the presence of one or more compounds indicates the binding of one or more of the compounds to L11/GAR.

The invention further encompasses a method for screening L11/GAR-binding compounds comprising the steps of: 1) incubating in vitro one or more compounds, a labeled known L11/GAR binding activity and an RNA comprising GAR RNA; 2) separating that fraction of the labeled known L11/GAR binding activity bound to the RNA from that fraction of the labeled known L11/GAR binding activity not bound to the RNA; and 3) detecting labeled known L11/GAR binding activity wherein a decrease in the level of the labeled known L11/GAR binding activity bound to the RNA in the presence of one or more compounds indicates that one or more of the compounds binds L11/GAR.

In one embodiment of the the method of screening L11/GAR-binding compounds, the

known L11/GAR binding activity is an antibiotic. In another embodiment the antibiotic is micrococcin. In a preferred embodiment the antibiotic is thiostrepton.

In another embodiment of the method of screening L11/GAR-binding compounds, the RNA comprising GAR RNA is contained within a ribosome.

In another embodiment of the method of screening L11/GAR-binding compounds, a plurality of compounds is screened for L11/GAR binding in a plurality of separate, simultaneous assays.

The invention further encompasses a method for screening L11/GAR-binding compounds comprising the steps of: 1) incubating in vitro one or more compounds with a translationally competent cell extract and a translatable RNA; and 2) detecting translation, wherein a decrease in the level of translation indicates binding of one or more of the compounds to L11/GAR.

In one embodiment, the translatable RNA encodes an enzyme and the step of detecting translation comprises detecting the activity of the enzyme.

In a preferred embodiment, the enzyme is luciferase.

In another embodiment, the translatable RNA is poly-U, and the step of detecting translation detects the incorporation of labeled phenylalanine into polyphenylalanine.

In another embodiment, the translationally competent cell extract comprises isolated ribosomes.

The invention further encompasses a method for screening L11/GAR-binding compounds comprising the steps of: 1) incubating in vitro one or more compounds, isolated 70S ribosomes, isolated EF-G and gamma-labeled GTP; and 2) detecting GTP hydrolysis wherein a decrease in GTP hydrolysis indicates one or more of the compounds binds L11/GAR.

The invention further encompasses a method for screening anti-bacterial compounds comprising the steps of: 1) incubating in vitro one or more compounds, a known L11/GAR binding activity and labeled RNA comprising GAR RNA; 2) separating that fraction of the labeled RNA bound to the known L11/GAR binding activity from that fraction of the labeled RNA not bound to the known L11/GAR binding activity; and 3) detecting labeled RNA, wherein a decrease in the level of the labeled RNA bound to the known L11/GAR binding activity in the presence of one or more compounds indicates that one or more of the compounds has anti-bacterial properties.

The invention further encompasses a method for screening anti-bacterial compounds comprising the steps of: 1) incubating in vitro one or more compounds, a labeled known L11/GAR binding activity and an RNA comprising GAR RNA; 2) separating that fraction of the labeled known L11/GAR binding activity bound to the RNA from that fraction of the labeled known L11/GAR binding activity not bound to the RNA; and 3) detecting labeled known L11/GAR binding activity wherein a decrease in the level of the labeled known L11/GAR binding activity bound to the RNA in the presence of one or more compounds indicates that one or more of the compounds has anti-bacterial properties.

In one embodiment of the the method of screening anti-bacterial compounds, the known L11/GAR binding activity is an antibiotic. In another embodiment the antibiotic is micrococcin. In a preferred embodiment the antibiotic is thiostrepton.

In another embodiment of the method of screening anti-bacterial compounds, the RNA comprising GAR RNA is contained within a ribosome.

In another embodiment of the method of screening anti-bacterial compounds, a plurality of compounds is screened for L11/GAR binding in a plurality of separate, simultaneous assays.

The invention further encompasses a method for screening anti-bacterial compounds comprising the steps of: 1) incubating in vitro one or more compounds with a translationally competent cell extract and a translatable RNA; and 2) detecting translation, wherein a decrease in the level of translation indicates that one or more of the compounds has anti-bacterial properties.

In one embodiment, the translatable RNA encodes an enzyme and the step of detecting translation comprises detecting the activity of the enzyme.

In a preferred embodiment, the enzyme is luciferase.

In another embodiment, the translatable RNA is poly-U, and the step of detecting translation detects the incorporation of labeled phenylalanine into polyphenylalanine.

In another embodiment, the translationally competent cell extract comprises isolated ribosomes.

The invention further encompasses a method for screening anti-bacterial compounds comprising the steps of: 1) incubating in vitro one or more compounds, isolated 70S ribosomes, isolated EF-G and gamma-labeled GTP; and 2) detecting GTP hydrolysis wherein a decrease in GTP hydrolysis indicates that one or more of the compounds has anti-bacterial properties. Further features and advantages of the invention are embodied in the following description of the invention and in the claims.

## BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows an overview of the secondary and tertiary structure of the GTPase activating region RNA from *Thermotoga maritima*: a) RNA secondary structure derived from the crystal structure. Lines indicate long-range base triples and the long-range 1088-1060 base pair; b) ribbon-and-stick schematic of the RNA tertiary structure (For clarity, protein L11 has



been omitted from view); c) same as (b), but the view is down the major groove of the 1095 stem to emphasize the compactness of the RNA fold. Figures 1b and 1c were made with the program RIBBONS (Carson, 1991).

Figure 2 shows selected details of the tertiary structure of the GTPase activating region RNA from *Thermotoga maritima*; in (a) and (b), the RNA backbone is represented by a ribbon and the phosphates are not shown: a) the ribose zipper that mediates the minor-groove to minor-groove association of the terminal stem and the 1082 hairpin loop (Hydrogen bonds are indicated by dotted lines); b) the major-groove to major-groove association of the 1067 and 1095 stem-loops, in a view emphasizing the high-five, S-turn, and dinucleotide platform motifs. The high-five motif consists of the long-range stacking of two bulged residues, U1061 and A1070. The S-turn comprises the inverted nucleotide U1060 and the bulged residue U1061. The dinucleotide platform motif consists of G1089 and U1090, on which the bulged residues G1071 and C1072 rest, as part of the long-range triples G1071-(G1091-C1100) and C1072-(C1092-G1099).

c) Geometries of the noncanonical base pairs and base triples. Top panel, the three major groove base triples in the core of the structure: G1089-(U1090-U1101), G1071-(G1091-C1100), and C1072-(C1092-G1099). Bottom left panel, the minor groove docking interactions (U1082-A1086)-(G1056-A1103) and A1085-(G1054-C1104). Bottom right panel, the long-range pair A1088-U1060. Figures 2a and 2b were made with RIBBONS (Carson, 1991); 2c with MOLSCRIPT (Kraulis, 1991).

Figure 3. RNA-metal ion interactions in the tertiary structure of the GTPase activating region

RNA from *Thermotoga maritima*: a) overview of the locations of the metal ions, showing that they are primarily in the interacting major grooves of the 1067 and 1095 stems. Magnesium ions are gold, cadmium ions are magenta, and the mercury ion is rose. b) close-up of the central cadmium ion that stabilizes sharp turns at the 1056-1057 and 1086-1087 phosphodiester linkages at the center of the 4-way junction. Direct ligation of the cadmium ion is indicated by solid lines, and second-shell ligation is indicated by dotted lines. Figure 3a was made with RIBBONS (Carson, 1991), and Figure 3b was made with MOLSCRIPT (Kraulis, 1991).

Figure 4 shows the RNA-L11 complex within the GTPase activating region from *Thermotoga maritima*: a) alignment of four widely divergent L11 sequences, together with a schematic of the protein's secondary structure. The sidechains of residues colored green participate in the hydrophobic core in the crystal structure. Residues involved in RNA binding are colored blue for side-chain contacts, red for main-chain contacts, or purple if both the side-chain and main-chain interact with RNA. Abbreviations: E. coli, *Escherichia coli* (eubacterium); T. marit, *Thermotoga maritima* (eubacterium); Sulf ac, *Sulfolobus acidocaldarius* (archaea); Sacc cer, *Saccharomyces cerevisiae* (eukaryote). The numbering is based on the *Thermotoga maritima* sequence present in the crystal structure. b) stereoview of the complex. The L11 N- and C-terminal domains are labeled. Note that the N-terminal domain straddles the interface of the 1067 and 1095 stem-loops. c) orthogonal stereoview of the complex. This view emphasizes the relatively loose association of the L11 N-terminal domain with the RNA. Figures 4b and 4c were made with RIBBONS (Carson, 1991).

Figure 5 shows Protein-RNA recognition within the GTPase activating region from *Thermotoga maritima*: a) schematic of RNA-CTD interactions observed in the crystal structure. Unusual RNA conformational features are also indicated (see inset for key). Water molecules that mediate protein-RNA interactions are indicated by a “W”. b) Detail of the recognition of the conserved long-range A1088-U1060 pair by conserved L11 residues Gly130 and Thr131 from helix 5, and by the N-terminus of helix 3. Figure 5b was made with MOLSCRIPT (Kraulis, 1991).

Figure 6 shows that the sites of mutations conferring resistance to thiostrepton and micrococcin are clustered around a cleft between the RNA and the proline-rich helix in the L11 N-terminal domain. Residues implicated in thiostrepton binding (A1067, A1095, and Pro22) are labeled. The position of Tyr61, which is protected by thiostrepton in protein footprinting experiments, is also indicated. Other labeled residues are those that confer micrococcin resistance (see text for details). The figure was made with RIBBONS (Carson, 1991).

Table II shows the atomic structure coordinates for the complex between ribosomal L11 protein and the GAR RNA as derived by X-ray diffraction from a crystal of L11 complexed with 23S rRNA nucleotides 1051-1108.

## DETAILED DESCRIPTION OF THE INVENTION

The invention is based on the discovery of the crystal structure of the ribosomal GAR from the hyperthermophilic eubacterium *Thermotoga maritima*, which is disclosed herein.

**Definitions:**

As used herein, the term “binding site” or “binding pocket” refers to a region of a protein or protein/RNA complex which binds or interacts with a particular compound. It is understood that the composition of the protein or RNA residues and/or the protein or RNA backbone, as well as the interaction of such moieties with their solvent including ions defines the specificity of the binding pocket.

As used herein, the term “exposed residue” refers to an amino acid or RNA residue which is located on the surface of a protein, RNA or RNA/protein complex.

As used herein the term “N terminus” or “N terminal lobe” or “NTD” when used in reference to L11 means amino acids 1-70 of L11.

As used herein, the term “C terminus” or “C terminal lobe” or “CTD” when used in reference to L11 means amino acids 76-141 of L11.

As used herein, the term “tether” or “tether sequence” when used in reference to L11 means amino acids 71 to 75 of L11.

As used herein, the term “flexible” when applied to a protein or RNA domain means that that domain allows one or more domains adjoining or flanking it to move or flex in space relative to the flexible domain.

As used herein, the term “backbone” or “backbone residue” when applied to an RNA molecule refers to the sugar-phosphate moieties that are covalently linked to form an RNA polymer. When applied to a protein molecule, “backbone” or “backbone residue” refers to the alternating N-C-C-N moieties of amino acids that are covalently linked to form a peptide polymer.

As used herein, the term “interface” means the point or surface at which two or more domains of one or more molecules associate with each other.

As used herein, the term “GAR” refers to the region of the ribosome responsible for activating the GTPase activity of translation elongation factors. The term “GAR RNA” refers to nucleotides 1051 to 1108 of E. coli 23S rRNA or to its functional and structurally equivalent from any other bacterial rRNA. As used herein, GAR RNA refers to the nucleotides including and limited to (i.e., an RNA molecule consisting of GAR RNA) nucleotides 1051 to 1108 of E. Coli 23S rRNA (or the functionally and structurally equivalent region in other bacterial rRNAs); or it refers to that nucleotide region (1051 to 1108) within a longer nucleotide sequence (i.e., an RNA molecule consisting essentially of GAR RNA) where the GAR RNA (nucleotides 1051 to 1108) is the only active region in the longer sequence (in terms of binding and/or another activity), whether the extra sequence be a homologous sequence from the 23S rRNA (short of the complete sequence) or a heterologous sequence; or it refers to the 1051 to 1108 region within a complete functional 23S rRNA (i.e., an RNA molecule comprising the GAR RNA).

As used herein, the term “L11/GAR” refers to the portions of L11 and GAR RNA which, when engaged in a complex, provide the L11/GAR binding site and/or activity, and preferably both the binding site and the activity. The term “L11/GAR” refers to a complex which consists of the ribosomal protein L11 and consists of the GAR RNA (nucleotides 1051 to 1108) in their native association; or it can refer to a complex consisting essentially of ribosomal protein L11 and consisting of or consisting essentially of or comprising GAR RNA (i.e., including other proteins which are inactive or do not otherwise affect the activity of the L11/GAR complex; or it can refer to a complex comprising ribosomal protein L11 and consisting of, consisting essentially of, or comprising GAR RNA. When ribosomal protein L11 is referred to, the complete protein is referred to; however, where an L11/GAR activity is referred to, the portion of L11 sufficient to provide the activity when associated in a complex

with GAR may be less than the complete L11 protein; “portion” referring to those combined L11 residues which provide for L11/GAR complex formation and activity, the portions being one or more of the N-terminal, C-terminal or tether regions, as defined herein, or any combination thereof.

“L11/GAR activity” may include one or more of the following: movement of the N-terminal lobe of L11; binding or displacement of thiostrepton or micrococin; RNA translation, translation elongation, inhibition of amino acid addition, GTPase activity, and/or inhibition of elongation factor G (EF-G)-dependent GTP hydrolysis.

As used herein, the term “known L11/GAR binding activity” refers to an activity known in the art to associate with the L11/GAR either in vitro or in vivo. Known L11/GAR binding activities include, but are not limited to, the binding of agents such as thiostrepton and micrococin.

As used herein, “stem loop” refers to a stretch of nucleic acid sequence on a single molecule comprising two lengths of sequence capable of forming hydrogen bonded base pairs with each other separated by a region which cannot participate in the same base pairing interaction, such that base pairing between the sequences capable of forming hydrogen bonded base pairs forms a loop of non-base paired nucleic acid consisting of the region which cannot participate in base pairing.

As used herein, the term “alpha helix” refers to a secondary structure arrangement of amino acids wherein hydrogen bonding between the C=O group of one peptide and the -NH group of the peptide bond four residues further down the same peptide polymer results in a right handed twist or helix formation.

As used herein, “four way junction” refers to a region in the tertiary structure of GAR RNA in which four helices interact simultaneously with each other, as defined by the crystal

structure coordinates given in Table II.

As used herein, the term “translationally competent cell extract” refers to any fraction of a cell lysate, including a whole cell lysate, which is capable of directing the RNA-dependent polymerization of peptide bonds.

As used herein, the term “translatable RNA” refers to an RNA which, when incubated with factors necessary for translation can direct the synthesis of acid-precipitable protein.

As used herein, the term “decrease” when used in reference to a level of labeled RNA, a level of known L11/GAR binding activity, a level of translation, or a level of GTP hydrolysis means that the detected level is reduced by at least 10%, and preferably by 20% to 50% or more.

As used herein, the term “anti-bacterial properties” refers to the ability of a particular compound to inhibit the growth of bacteria. A compound can be said to have anti-bacterial properties if the rate of bacterial cell proliferation is reduced by at least 50%, and preferably by more than 50%.

As used herein, the term "naturally occurring amino acids" means the L-isomers of the naturally occurring amino acids. The naturally occurring amino acids are glycine (G, Gly), alanine (A, Ala), valine (V, Val), leucine (L, Leu), isoleucine (I, Ile), serine (S, Ser), methionine (M, Met), threonine (T, Thr), phenylalanine (F, Phe), tyrosine (Y, Tyr), tryptophan (W, Trp), cysteine (C, Cys), proline (P, Pro), histidine (H, His), aspartic acid (D, Asp), asparagine (N, Asn), glutamic acid (E, Glu), glutamine (Q, Gln), gamma-carboxyglutamic acid, arginine (R, Arg), ornithine and lysine (K, Lys). Unless specifically indicated, all amino acids referred to in this application are in the L-form.

As used herein, the term "unnatural amino acids" means amino acids that are not naturally found in proteins. Examples of unnatural amino acids used herein include racemic

mixtures of selenocysteine and selenomethionine.

The term "positively charged amino acid" includes any naturally occurring or unnatural amino acid having a positively charged side chain under normal physiological conditions. Examples of positively charged naturally occurring amino acids are arginine, lysine and histidine.

The term "negatively charged amino acid" includes any naturally occurring or unnatural amino acid having a negatively charged side chain under normal physiological conditions. Examples of negatively charged naturally occurring amino acids are aspartic acid and glutamic acid.

The term "hydrophobic amino acid" means any amino acid having an uncharged, nonpolar side chain that is relatively insoluble in water. Examples of naturally occurring hydrophobic amino acids are alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine.

The term "hydrophilic amino acid" means any amino acid having an uncharged, polar side chain that is relatively soluble in water. Examples of naturally occurring hydrophilic amino acids are serine, threonine, tyrosine, asparagine, glutamine, and cysteine.

As used herein, a "competitive" inhibitor is one that inhibits GAR activity by binding to the same kinetic form of the GAR as its accessory factors bind--thus directly competing with the accessory factors for the active site of the GAR. Competitive inhibition can be reversed completely by increasing the accessory factor concentration.

As used herein, the term "kinetic form" of the GAR means the condition of the GAR when either bound to an accessory factor or not, and in either its active or inactive state. That is, a kinetic form can be any conformation the GAR can assume under physiological conditions.



As used herein, the term "accessory factor" means an endogenous factor or protein that interacts with the L11/GAR. As used herein, EF-G is included in the term "accessory factor".

As used herein, an "uncompetitive" inhibitor is one that inhibits GAR activity by binding to a different kinetic form of the GAR than do the accessory factors. Such inhibitors bind to GAR already bound with the accessory factor and not to the accessory factor-free GAR. Uncompetitive inhibition cannot be reversed completely by increasing the accessory factor concentration.

As used herein, the term "co-complex" means L11 protein in covalent or non-covalent association with GAR RNA. As used herein, a co-complex may also encompass accessory factors and/or inhibitors or activators complexed with L11 or L11/GAR RNA.

As used herein, the terms "associates with" or "interacts with" refers to a condition of proximity between a chemical entity or compound, or portions thereof, with another chemical entity, compound or portion thereof. The association or interaction may be non-covalent --wherein the juxtaposition is energetically favored by hydrogen bonding or van der Waals or electrostatic interactions-- or it may be covalent.

The term "beta-sheet" refers to the conformation of a polypeptide chain stretched into an extended zig-zig conformation. Portions of polypeptide chains that run "parallel" all run in the same direction. Polypeptide chains that are "antiparallel" run in the opposite direction from the parallel chains.

As used herein, the term "target" means a region of the L11/GAR complex, as defined by the crystal structure coordinates of Table II, which when bound by a candidate inhibitor or activator results in inhibition or activation of L11/GAR function.

As used herein, the term "modulate" refers to a change, either an increase or a

decrease in some activity.

As used herein, the term “modulator” means a compound that modulates some activity.

As used herein, the term “inhibits” or “decreases” means that a candidate modulator reduces the activity of the L11/GAR. A candidate modulator may be said to inhibit or decrease activity if the activity of L11/GAR as measured by inhibition of GTP hydrolysis and/or translational activity is reduced by more than 50% in the presence of 50 uM or less of inhibitor compared to values obtained in the absence of inhibitor. Candidate modulators will preferably inhibit by more than 50% the presence of 10 uM or less of inhibitor and most preferably in the presence of 1 uM or less of inhibitor.

As used herein, the term “activates” or “increases” means that a candidate modulator raises the activity of the L11/GAR. A candidate modulator may be said to activate or increase activity if the activity of L11/GAR as measured by an increase of GTP hydrolysis by more than 50% in the presence of 50 uM or less of activator compared to values obtained in the absence of activator. Candidate modulators will preferably activate by more than 50% in the presence of 10 uM or less of inhibitor and most preferably in the presence of 1 uM or less of inhibitor.

As used herein, the term "structure coordinates" refers to mathematical coordinates derived from mathematical equations related to the patterns obtained on diffraction of a monochromatic beam of X-rays by the atoms (scattering centers) of an L11/GAR RNA complex in crystal form. The diffraction data are used to calculate an electron density map of

the repeating unit of the crystal. The electron density maps are used to establish the positions of the individual atoms within the unit cell of the crystal.

As used herein, the term "heavy atom derivatization" refers to the method of producing a chemically modified form of a crystal of L11/GAR RNA. In practice, a crystal is soaked in a solution containing heavy metal atom salts, or organometallic compounds, e.g., methyl mercury nitrate, lead chloride, gold thiomalate, thimerosal or uranyl acetate, which can diffuse through the crystal and bind to the surface of the protein. The location(s) of the bound heavy metal atom(s) can be determined by X-ray diffraction analysis of the soaked crystal. This information, in turn, is used to generate the phase information used to construct three-dimensional structure of the protein or protein:RNA complex (Blundel, T. L. and N. L. Johnson, 1976, Protein Crystallography, Academic Press).

Those of skill in the art understand that a set of structure co-ordinates determined by X-ray crystallography is not without standard error. For the purpose of this invention, any set of structure coordinates for an L11/GAR RNA complex that has a root mean square deviation of protein backbone atoms (N, C $\alpha$ , C and O) of less than 0.75 when superimposed on the structure coordinates of Table II, using backbone atoms, shall be considered identical.

The term "unit cell" refers to a basic parallelepiped shaped block. The entire volume of a crystal may be constructed by regular assembly of such blocks. Each unit cell comprises a complete representation of the unit of pattern, the repetition of which builds up the crystal. Using the structure coordinates of the L11/GAR RNA complex provided by this invention, molecular replacement may be used to determine the structure coordinates of a crystalline mutant or homologue of the L11/GAR RNA complex or of a different crystal form of the L11/GAR RNA complex.

## Detailed Description of the High Resolution Structure of the L11/GAR complex.

The GAR RNA from the *T. maritima* 23S rRNA consists of nucleotides 1111-1168, which correspond to nucleotides 1051-1108 in the *E. coli* sequence. Hereafter, the *E. coli* numbering will be used in order to facilitate comparison with the available biochemical and genetic data. As described in detail in Example 1, crystals of the GAR RNA complexed with ribosomal protein L11 from *T. maritima* were prepared and used to solve the structure to 2.6 Å resolution using multi-wavelength anomalous diffraction on a mercury derivative of the crystal. Data collection, phasing and refinement statistics are shown in Table I. The

asymmetric unit in the crystal consists of two 1:1 L11-RNA complexes stacked in a head-to-head manner. The two complexes are nearly identical except for a subtle bend in the terminal three base pairs of the RNA, and a difference in the degree of disorder of the two L11 N-terminal domains. Several observations strongly suggest that the conformation observed in the crystal structure is extremely similar to the structure of the GAR *in situ* in the ribosome. The RNA contains all of the predicted secondary structure; the two complexes in the asymmetric unit are virtually identical; and, most significantly, the structure explains most of the large body of experimental data on this system.

### *Structure of the GAR RNA*

The predicted secondary structure of the GAR RNA (Glitz et al., 1981; Noller et al., 1981) is almost identical to that derived from the crystal structure (Figure 1a). The RNA secondary structure contains four double-helical segments, referred to as the terminal stem (defined by nucleotides (nt) 1051-1056 base paired with nt 1103-1108), the 1067 stem-loop (defined by nt 1062-1076), the 1082 hairpin (defined by nt 1082-1086) and the 1095 stem-loop (defined by nt 1090-1101).

In the tertiary structure, the terminal stem stacks on the 1095 stem-loop, and the 1067 stem-loop stacks on the 1082 hairpin. Thus the four double-helical segments stack pairwise to form two extended helical subdomains. These two subdomains have irregular yet complementary shapes, so that the entire GAR RNA folds into a single compact globular domain (Figures 1b, c). The helical subdomains associate in a roughly parallel fashion, with the terminal stem packed against the 1082 hairpin, and the 1067 and 1095 stem-loops packed against each other. Bulged-out residues in the 1067 and 1095 stem-loops mediate long-range tertiary interactions between the two subdomains. The fold requires two sharp turns in the backbone at the 1056-1057 and 1086-1087 phosphodiester linkages in the center of the junction, where the chain crosses over from one helical subdomain to the other. The molecule also contains a relatively large number of well-ordered metal ions that are integral to the structure.

#### *A ribose zipper joins the terminal stem and the 1082 hairpin*

The association of the terminal stem with the 1082 hairpin occurs via their minor grooves. This rather intimate packing is stabilized primarily by a dense network of hydrogen bonds between the riboses of nucleotides A1084-A1086 and C1104-A1106 (Figure 2a). A similar structural motif has been observed in the P4-P6 domain of the group I intron, and has been referred to as a ribose zipper (Cate et al., 1996). At the center of the four-way junction, the 2' OH of A1086 appears to be a particularly crucial component of the ribose zipper. It makes hydrogen bonds to A1103 N1 and G1056 2' OH, and also directly ligates a crucial central cadmium ion (see below). A1086 has an unusual *syn* conformation that is necessary for the very tight packing of its sugar against the G1056-A1103 pair, and for the reverse-Watson-Crick geometry of the U1082-A1086 pair (Figure 2c). Another noteworthy feature of

the ribose zipper is a minor groove A-(G-C) triple involving nucleotides A1085, G1055 and C1104 (Figure 2c). This minor-groove triple has also been found previously in large RNA tertiary folds (Cate et al., 1996; Ferre-D'Amare et al., 1998).

*Intimate association of the 1067 and 1095 stem-loops by reciprocal donation of bulges*

The interaction between the 1067 and the 1095 stem-loops occurs primarily in their major grooves and is mediated largely by a reciprocal donation of highly conserved bulged-out bases. This unusually intimate major-groove packing is the primary reason for the compactness of the overall fold, and it requires substantial distortions from regular helical geometry. This portion of the structure contains a large number of tertiary interactions, some of which are novel structural motifs.

The 1095 stem donates a bulged-out base, A1088, to a pocket created by a distortion in the 1067 stem (Figure 1). A1088 forms a universally conserved reverse-Hoogsteen pair with U1060 (Figure 2c). Because of steric constraints, A1088 must be in the *syn* conformation, which together with the reverse-Hoogsteen pairing geometry requires that U1060 must be flipped over. The inversion of U1060 is in turn facilitated by bulging out of the base of U1061. This inversion-bulge, or S-turn motif, has an S-shaped backbone conformation that has been observed previously (Szewczak et al., 1993; Wimberly, 1994; Wimberly et al., 1993). The insertion of A1088 also requires that residues A1077 and U1078 are unpaired and rotated out to open up the pocket. The unpaired conformation of these residues is stabilized by three hydrogen bonds to the sugar-phosphate backbone of the 1095 stem loop at A1088 and G1089. Two of these hydrogen bonds are to the base of A1077 which explains its universal conservation.

The reciprocal donation of a bulge from the 1067 stem-loop to the 1095 stem involves

nucleotides G1071 and C1072, which form two novel interdomain base triples with the base pairs G1091-C1100 and C1092-G1099 respectively (Figures 2b, c). Within the 1095 stem loop, nucleotides G1089-(U1090-U1101) also form a triple (Figure 2c), with G1089 acting as a stacking platform for the other two triples (Figure 2b). The stacking of G1071 on G1089 is further stabilized by hydrogen bonds between the 1089 2'OH and 1071 N3, and between the 1071 2' OH and the 1089 phosphate. These three base triples explain the sequence conservation of all these residues. The 1072-(1092-1099) triple was previously predicted and subsequently experimentally confirmed, although the geometry proposed for the triple (Conn et al., 1998) differs from that seen in the crystal structure.

#### *The 1067 and 1095 hairpin loops*

The highly conserved 1067 hairpin loop consists of two parts, a hairpin portion (U1066-A1069) that stacks on the sheared U1065-A1073 pair, and a three-nucleotide bulge (A1070-C1072) that participates in two different long-range tertiary interactions. The hairpin portion has a conformation commonly found in small hairpin loops, with a U-turn motif (Quigley and Rich, 1976) at U1066 and regular stacking of A1067-G1068-A1069. A1069 stacks on A1073, and its 2' OH hydrogen bonds to the N3 of U1065, thereby stabilizing the location of the 1069 sugar as well as the sheared geometry of the U1065-A1073 pair. The three-nucleotide bulge has a corkscrew-like conformation in which A1070 is bulged to one side, and G1071 and C1072 are bulged into the major groove of the 1095 stem-loop. A1070 makes a novel long-range stacking interaction with U1061 which will be referred to herein as a “high-five” motif (Figure 2b), while 1071 and 1072 participate in the long-range base triples described above. The high-five motif makes several hydrogen-bonding and van der Waals interactions with the 1095 hairpin loop, thereby stabilizing the relative orientations of





junction.

Despite the accelerating pace of RNA structure determination, extremely little is known about RNA tertiary structure because only about five RNA folds have been determined. The crystal structure of the GAR RNA reveals an unexpectedly complex and compact fold that contains both well-known and novel structural motifs. The GAR RNA is in fact the most compact RNA structure yet reported, exposing only 138 Å<sup>2</sup> of solvent accessible surface area per nucleotide (Nicholls et al., 1991). This extreme compactness is a result of extensive tertiary interactions along the entire length of the structure, in both the major and minor grooves. The other relatively compact known RNA folds exhibit primarily minor-groove packing (e.g., the P4-P6 domain of the group I intron) or primarily major-groove packing (e.g., tRNA), and are therefore less efficiently folded. It is probable that very efficient packing of RNA will be found to be common in the ribosome.

The crystal structure explains the molecular basis for a number of important mutagenesis results. In particular, the RNA residues most sensitive to mutation are involved in tertiary interactions. For example, mutation of any of the universally conserved residues within the A1085-G1055-C1104 triple, a crucial part of the ribose zipper joining the terminal stem and the 1082 hairpin, dramatically destabilizes the RNA structure and greatly reduces the affinity for L11 (Lu and Draper, 1995). Mutation of C1072 to U within the 1072-(1092-1099) triple destroys the RNA tertiary structure, which demonstrates the energetic importance of this triple. Finally, the unusual observation that U1061A and U1061G mutants are more stable (Lu and Draper, 1994; Lu and Draper, 1995) is explained by the 1061-1070 “high five” tertiary stacking motif, since purine stacking is more stable than pyrimidine stacking.

*Stabilization of the RNA tertiary structure by metal ions*

The crystal structure also reveals important new information about how metal ions interact with and stabilize unusual RNA structures. Biochemical experiments suggest that the GAR RNA contains relatively high affinity binding sites for two divalent cations (Bukhman and Draper, 1997) and one  $K^+$  or  $NH_4^+$  ion (Wang et al., 1993). The crystal structure reveals no fewer than seven magnesium sites and two cadmium sites, most of which stabilize the close approach of phosphates in the interacting major grooves of the 1067 and 1095 stem-loops. The metal-ion stabilization of the 1070-1072 bulge conformation is qualitatively similar -- though different in detail -- to that seen in the A-rich bulge of the P4-P6 domain of the group I intron (Cate et al., 1996). The striking structural role played by the central cadmium ion suggests that this site corresponds to one of the thermodynamically important ions. While more experiments will be necessary to test this hypothesis, it is worth noting that this cadmium ion is one of the two sites in the structure that ligates a guanosine N7. Both  $Mn^{++}$  and  $Cd^{++}$  preferentially bind to guanosine N7, and it has been observed that  $Mn^{++}$  stabilizes the tertiary structure more than other divalent cations (Bukhman and Draper, 1997).

*The major-groove dinucleotide platform: a generalization of the adenosine platform*

The crystal structure also reveals a new variant of a known tertiary structure motif, the adenosine platform. In the structure of the P4-P6 domain, two successive adenines adopt a coplanar conformation -- an adenosine platform -- that serves as a stacking platform for a long-range tertiary interaction (Cate et al., 1996). In the GAR structure, two successive nucleotides, G1089 and U1090, adopt the same conformation seen in the adenosine platform (Figure 2C). The two bases are coplanar, with a single N2-O4 hydrogen bond between them, and they also serve as a stacking platform, for the 1071-1072 bulge involved in base triples (Figure 2B). There are, however, some differences between the GU platform seen here and

the AA platform. In the P4-P6 structure, the motif is displayed in the minor groove rather than in the major groove, as is seen here. Moreover, in the P4-P6 structure it is the 3' adenosine upon which the long-range stacking interaction occurs, while here G1071 rests upon the 5' residue of the motif, G1089. Finally, the tertiary stacking interaction occurs on opposite faces of the motif in the two structures. Despite these differences, the near-identity of the conformations and functions of the motifs in these two structures leads to the suggestion that the motif be referred to as a "dinucleotide platform", since it is clearly not restricted to adenosines. The few available data suggest that a GU dinucleotide platform may generally be more stable than an AA platform for major groove display. In the GAR, residues 1089 and 1090 are strictly conserved as either GU or AA, but mutation from AA to GU results in a significant stabilization of the RNA tertiary structure (Lu and Draper, 1994; Lu and Draper, 1995). The major-groove GU dinucleotide platform motif has also been found in small RNA structures lacking tertiary interactions (Szewczak et al., 1993; Wimberly et al., 1993), which suggests that in large structured RNAs, the GU dinucleotide platform may in some cases function as a pre-formed stacking platform supporting major-groove base triples.

#### *Methylmercury as a phasing vehicle for RNA crystal structures*

Surprisingly, the primary mercury site used in phasing is not near a cysteine of L11, but is located 2.4 Å from the N3 atom of U1061, consistent with a covalent mercury-uridine N3 bond. A similar, minor mercury site at U1078 is also visible in the anomalous difference Fourier map. Although most mercury adducts of pyrimidines have been obtained at the O4 or 5 positions of the base, a mercury 1-methylthymine adduct at N3 has been obtained at alkaline pH (Kosturko et al., 1974), and methylmercury salts have been shown to denature AT-rich DNA, consistent with reaction at thymine N3 (Gruenwedel and Davidson, 1966;

Gruenwedel and Davidson, 1967). Uracil is often preferred at bulge sites in RNA, so many larger RNA structures may contain solvent-accessible uracils. Therefore, methylmercury derivatization of RNA under native conditions, either prior or subsequent to crystallization, may be a generally useful method for obtaining heavy atom derivatives of RNA crystals, without the laborious incorporation of sulfur-containing ribonucleotides.

### *The structure of ribosomal protein L11*

Ribosomal protein L11 consists of two globular domains connected by a linker region. The secondary structure and a sequence alignment of the protein are shown in Figure 4a, and the tertiary fold is shown in Figures 4b and 4c in the context of the complex. As described below, there is some flexibility between the two domains, but the linker is short and it contains two conserved prolines (73 and 74) that provide inherent rigidity. Also, the domain interface consists primarily of conserved hydrophobic residues, notably Met52, Ile53, Pro55, Pro73 and Phe77. These observations suggest that relative orientation of the two domains has not been greatly perturbed by crystal packing requirements.

The structure of the L11 N-terminal domain (NTD) has not been previously reported. It consists of two helices packed against the concave surface of a three-stranded antiparallel beta sheet, with an overall  $\beta 1-\alpha 1-\alpha 2-\beta 2-\beta 3$  topology. The N-terminal 7 residues are disordered. One of the most distinctive and conserved regions of the L11 molecule is the proline-rich helix 1, which appears to have a crucial functional role, as described below. The electron density for this helix was weak, and the register of the sequence in this helix may be in error by one residue. The average main-chain B-factor for the domain is 72 Å<sup>2</sup> (for comparison, the average B-factor of the C-terminal domain (CTD) is 24 Å<sup>2</sup>), indicating rigid

body movement of the NTD within the crystal. This flexibility is consistent with the rather limited interactions seen between the NTD and other parts of the structure, and may have functional implications (see below).

The structure of the CTD is in good agreement with the previously determined NMR structures of the CTD, both in isolation (Markus et al., 1997; Xing et al., 1997) and in the context of the L11-RNA complex (Hinck et al., 1997). The domain consists of a three-helical bundle and a short parallel two-stranded  $\beta$ -ribbon, with an overall  $\alpha 3$ - $\beta 4$ - $\alpha 4$ - $\alpha 5$ - $\beta 5$  topology. All five secondary structure elements contribute to a conserved hydrophobic core. The domain is characterized by two extended loops that are disordered in the absence of the RNA, but which have defined structures in the complex.

#### *The RNA-protein interaction*

The two domains of L11 are very unequally associated with RNA. The CTD-RNA interface covers over 1700 Å<sup>2</sup> of solvent accessible surface area, while the NTD-RNA interface is less than 100 Å<sup>2</sup>. This difference is consistent with the observation that the RNA-binding affinity of the CTD is essentially the same as that of the full-length protein (Xing and Draper, 1996).

The CTD binds the minor groove of the 1067 stem (Figures 4b, c), which is bent and flatter than the minor groove of a canonical A-form double helix. The RNA-binding surface of the CTD consists of one face of helix 5, the N-terminal end of helix 3, and loops 6 and 7 that flank helix 5. Helix 5 is positioned lengthwise in the minor groove, and the flanking loops 6 and 7 extend this minor groove binding surface and also interact with the sugar-phosphate backbones on either side of the groove. A summary of the CTD-RNA interactions observed in the crystal structure (Figure 5a) emphasizes that the recognition of the RNA

minor groove by L11 involves primarily interactions between the protein backbone and the RNA 2' OH moieties. Approximately half of the RNA-CTD hydrogen bonds involve a main-chain amide or carbonyl, and over half of the 2'OH groups in the CTD footprint are hydrogen-bonded to the protein. This preponderance of protein backbone-RNA backbone interactions indicates that overall shape complementarity between the RNA and protein must be an important determinant of specificity.

Although binding appears to depend less on electrostatic interactions than on shape complementarity, there are a number of important salt bridges between basic sidechains and phosphate groups: lysines 93, 126 and 133 and Arg94 interact with one side of the minor groove, and lysines 80, 87 and 112 with the other side. In the former group, the sidechains are splayed away from protein, and the hydrophobic part of the sidechain contributes to surface complementarity with the RNA. Sidechains at the N-terminus of  $\alpha 5$  and within loop 7 make particularly intimate contact with the RNA, notably Ile127 and Asn117. Asn117 points directly into the minor groove making a number of hydrogen bonding interactions, and is one of the few sidechains that formally “reads” the local RNA sequence. Two of the most important recognition elements in the RNA are the universally conserved long-range pair U1060-A1088 and the surrounding RNA internal loop that distorts to accommodate the insertion of A1088. Significantly, the RNA footprint of helix 5 encompasses this entire region of distorted RNA. The importance of the U1060-A1088 pair for L11 specificity is shown by the extremely high conservation of Gly130 and Thr131 to which these bases are hydrogen-bonded (Figure 5b).

The NTD bridges the interface between the 1067 and 1095 stem-loops, and it makes only a few specific interactions with the RNA (Figure 4). Although its association with RNA

is somewhat tenuous, which might be a result of its binding mode having been altered by crystal packing requirements, the high sequence conservation of the NTD residues interacting with RNA suggests that the binding mode observed in the crystal structure is relevant to the structure of the complex in solution. Moreover, as described above, the structure of the NTD-CTD interface also suggests that the orientation of the NTD has not been greatly perturbed by crystal packing. The NTD residues interacting with RNA include Lys10, Gln12, Gln30 and Lys71. Lys10 makes both main-chain and side-chain interactions with the RNA, and Gln 30 probably interacts specifically with A1095. There is also electron density interacting with the Watson-Crick face of C1097, but it is not clear whether this density arises from the NTD; examination of an anomalous difference Fourier map reveals that some of this density must correspond to a mercury or cadmium site. Finally, although the proline-rich sequence in helix 1 is surface-exposed, highly conserved, and in the correct orientation for possible interactions with factors or antibiotics, it is close to but not in direct contact with RNA.

#### *The thiostrepton/micrococccin binding site*

A1067 and A1095, at the ends of their respective stem-loops, have both been implicated in the binding of the antibiotics thiostrepton and micrococccin. Modification of A1067 by 2'-O methylation (Cundliffe and Thompson, 1979; Thompson et al., 1982) or transversion mutations at either site (Rosendahl and Douthwaite, 1994) confers thiostrepton resistance. It has also been shown that thiostrepton affects the reactivity of both A1067 and A1095, suggesting that these two sites are close together (Rosendahl and Douthwaite, 1994) as indeed they are in the crystal structure. As for the role of L11 in antibiotic binding, it is known that L11 is required for high affinity binding of thiostrepton to the RNA, and that binding of L11 and thiostrepton to the RNA is cooperative. Thiostrepton has a much weaker

affinity for the RNA alone ( $K_d = 0.4 \mu\text{M}$ ), and it does not bind isolated L11 (Thompson et al., 1979). Two sites within the NTD of the protein have been implicated in this interaction: the mutations Pro22Ser and Pro22Thr confer thiostrepton resistance, while the antibiotic protects Tyr61 (Tyr62 in *E. coli*) in protein footprinting experiments (Porse et al., 1998). Recently, mutations that confer resistance to micrococcin have also been mapped to the NTD of L11 between residues 22 and 32 (Porse et al., 1999). All of these sites are located on a small surface of the NTD, near A1067 and A1095 on the RNA (Figure 6). A prominent feature of this surface is the distinctive and highly conserved proline-rich helix, while Tyr61 is over 20 Å distant. The clustering of these sites of antibiotic resistance mutations, together with the cooperative binding data, strongly suggest that the antibiotics bind to the cleft between the RNA and the proline-rich helix 1 of the NTD.

The structure of the C-terminal domain (CTD) was previously determined by NMR in both the free (Markus et al., 1997; Xing et al., 1997) and RNA-bound (Hinck et al., 1997) forms. Our crystal structure of the CTD is similar to that of the RNA-bound form determined by NMR, except for the conformation of the large RNA-binding loop 6 which is poorly determined in the NMR studies (Hinck et al., 1997). The mean C $\alpha$  root mean square difference (RMSD) for the crystal structure vs. NMR ensemble is 2.7 Å overall, or 1.6 Å when residues 86-97 of loop 6 are excluded. For comparison, the mean RMSD within the ensemble of NMR structures is 2.3 Å for main chain atoms.

Many ribosomal proteins show structural similarities to families of DNA- and RNA-binding proteins (Ramakrishnan and White, 1998). It was noted from the NMR structure that the CTD of L11 has a homeodomain-like fold (Markus et al., 1997; Xing et al., 1997), and further NMR studies on the complex suggested that the CTD uses the typical homeodomain



helix to bind RNA (Hinck et al., 1997). Although the crystal structure reveals that this helix is indeed intimately associated with the RNA, its interaction does not bear any similarity to the base-specific recognition of a major groove by the homeodomains. Regarding the NTD, its overall  $\alpha + \beta$  fold is similar to that seen in many other RNA-binding proteins (Ramakrishnan and White, 1998), but its  $\beta$ - $\alpha$ - $\alpha$ - $\beta$ - $\beta$  topology has not yet been observed in an RNA-binding protein.

### ***RNA-protein interaction***

The L11-GAR RNA interaction has been probed by biochemical and NMR methods, and the crystal structure is in good agreement with the results of these studies, including a rather weak interaction between the RNA and the NTD. The RNA surface covered by the CTD corresponds fairly well to the residues protected by the binding of full-length L11 as shown by hydroxyl radical footprinting experiments (Rosendahl and Douthwaite, 1993). The RNA-binding surface of the CTD has been mapped by NMR chemical shift changes and relaxation studies (Hinck et al., 1997), and again the agreement with the crystal structure is excellent. The observation that L11 recognizes the RNA primarily by shape complementarity rather than by a sidechain-base reading of the RNA sequence is not surprising considering that the interaction occurs primarily via the minor groove. The interaction agrees with the prediction that relatively few highly conserved CTD residues would make specific sidechain contacts with RNA (Xing et al., 1997). However, the related prediction that RNA binding by the CTD would not involve extensive recognition of the RNA bases is incorrect, as most of the base pairs are recognized by either hydrogen bonding or hydrophobic interactions. However, most of these hydrogen bonds occur via main chain amides or carbonyls, rather than side chains. Finally, it is worth noting that L11 does not directly recognize the bulged-

out nucleotides, which have previously been proposed as specificity determinants in ribosomal RNA-protein complexes.

Biochemical experiments have shown that L11 stabilizes the tertiary structure of the RNA, and that this is a property of the CTD (Draper and Xing, 1995; Xing and Draper, 1995). Since nearly all of the direct RNA-protein contacts within the complex are to the 1067 stem, the resulting stabilization of the RNA tertiary structure appears to be indirect. The binding of one face of helix 5 with both strands of the 1067 stem is extensive and universally conserved, and this interaction must be particularly important for stabilization of the RNA tertiary structure. Consistent with a crucial role in RNA binding, helix 5 contains most of the mutation sites that have the greatest adverse effect on binding affinity (T131V, G130A, K126A, and S134A) (Xing et al., 1997). As for the RNA-binding loops 6 and 7, both are disordered when not bound to RNA (Markus et al., 1997), but they are highly ordered in the complex, and their conformations match the groove surface perfectly. The loops contain conserved structural features, which are important in the complex and which may predispose them for RNA-binding. Although it makes many interactions with RNA and contains the other two sites most sensitive to mutation (G88P and P92G), the longer RNA-binding loop 6 is relatively poorly conserved between kingdoms, with the bacterial and archaeal loops differing significantly from the eukaryotic loops (Figure 4A). This variability in the protein sequence correlates with variability between phylogenetic kingdoms in the base-pairing of the upper portion of the 1067 stem.

#### *The NTD as a molecular switch*

Prior to these structural studies, the molecular basis for cooperative binding within the RNA-L11-thiostrepton ternary complex was unknown. The crystal structure now provides a

very straightforward explanation that also rationalizes the particular importance of the L11 NTD. The model also provides insights into how the GAR might function as a molecular switch.

The putative thiostrepton/micrococcin binding site is centered on a small gap between helix 1 of the NTD and the 1067/1095 region of the RNA (Figure 6). The antibiotics are proposed to bind within this gap, possibly enlarging it somewhat, making specific interactions with the RNA on one side and further interactions with the NTD on the other side. In the absence of the NTD, the antibiotic's binding affinity would be greatly compromised, thus explaining the importance of the NTD for antibiotic binding (Xing and Draper, 1996). An alternative proposal, that thiostrepton binds directly only to the RNA and that this RNA conformation requires the presence of the NTD, is unlikely because the NTD does not appear to stabilize the RNA tertiary structure significantly, and because the NTD sites of resistance mutations are not in contact with the RNA. In a model that better accounts for previously known data and agrees with the crystal structure reported herein, the mechanism for the resistance to thiostrepton in Pro22 mutants would be a disruption of direct thiostrepton-Pro22 interaction. A similar mechanism must hold true for the micrococcin sites given the more recent data (Porse et al., 1999). Regarding the details of the interaction of thiostrepton and micrococcin with RNA, we note that these antibiotics contain an array of thiazole rings that resembles the array of prolines in the conserved proline-rich NTD helix.

The data disclosed herein suggests a potential mechanism of thiostrepton inhibition of factor-dependent GTPase activity involves restriction or "trapping" of one of the many conformational states that must occur during elongation (Cundliffe, 1986) by the antibiotic. In their analysis of the effects of the Pro22Ser and Pro22Thr mutations, Porse *et al.* (1998)

suggest that thiostrepton binding may affect the ability of the L11 NTD to undergo a conformational change, an idea which merits closer examination in light of the crystal structure. In the structure, the CTD is rather firmly anchored to one of the two RNA subdomains, while the NTD is somewhat tenuously bound across the RNA subdomain-subdomain interface. Even in the absence of other data, this overall architecture suggests that the NTD may function as a molecular switch that reversibly associates with the GAR RNA during the elongation cycle. In light of the other data -- in particular the cooperative binding of thiostrepton and full-length L11 to RNA, and the clustering of antibiotic resistance mutations to the cleft defined by A1067/A1095 and the proline-rich NTD helix -- it appears even more likely that the NTD functions as a molecular switch, and that the thiazole antibiotics work by binding to the NTD-RNA interface, thereby preventing the NTD from switching between RNA-bound and RNA-free states. It is possible that the switch is coupled to, or triggered by, the binding of elongation factors. It is important to note that the NTD itself cannot provide the actual GTPase enhancing activity since L11 is not required for viability in *E. coli* (Stöffler et al., 1980). Therefore, the switch appears likely to function by controlling either the accessibility or the conformation of the GAR RNA.

This switch hypothesis could also explain why EF-Tu and IF2 do not footprint the 1067/1095 region of RNA, while EF-G does, even though all these factors interact with the sarcin/ricin loop (Moazed et al., 1988). The sarcin/ricin loop is known to bind to a nearby (Wilson and Noller, 1998) but distinct (Munishkin and Wool, 1997) site on EF-G. The EF-Tu-tRNA complex is similar in structure to EF-G, and the similarity is thought to be a case of molecular mimicry, with the factors binding to the same general region of the ribosome (Nissen et al., 1995). Thus the footprinting differences could be explained if EF-Tu and IF2

recognize a different conformation of the switch than EF-G does. This reasoning suggests that the two conformations of the GAR molecular switch correspond to different functional states of the ribosome.

The structure features a complex and very compact RNA fold stabilized by many bound metal ions, by a dense network of RNA tertiary interactions, and by extensive interactions with the protein. The overall architecture of the complex suggests that the N-terminal domain functions as a molecular switch, either by facilitating changes in the tertiary structure of the GAR RNA, or by controlling access to the RNA. Thiostrepton and micrococccin are proposed to bind to the NTD-RNA interface, thus locking the switch and disrupting GAR function.

### **Uses of the Crystal Structure Coordinates of the L11/GAR Complex**

One approach enabled by the X-ray crystal structure disclosed herein is the use of the crystal coordinates for the rational design of GAR activity modulators, either de novo or by modification of known compounds. The modulators identified through use of the crystal structure coordinates will be useful for altering the rate of bacterial protein synthesis, and thereby the rate of bacterial cell growth. It is expected that, for example, an inhibitor of GAR function will inhibit bacterial cell proliferation, and will thus potentially have immediate medical usefulness.

One of skill in the art may use the structure data disclosed herein and the

computer-modeling techniques described herein to develop models of target domains also selected through analysis of the crystal structure data (see below). These models can be used to provide a detailed analysis of the binding surfaces, including factors such as van der Waals contacts, electrostatic interactions and hydrogen-bonding opportunities. This information is then used with computer simulation techniques to map the favorable interaction positions for functional groups such as protons, hydroxyl groups, amine groups, divalent cations, aromatic and aliphatic functional groups, acetamide, methanol, etc. These groups may then be designed into a synthetic ligand.

The L11/GAR structure coordinates may be used to screen computationally small molecule data bases for chemical entities or compounds that may bind in whole, or in part, to the L11/GAR, to GAR, or to L11.

In addition, because the L11/GAR RNA complex may be crystallized in more than one crystal form (e.g, as a co-crystal with another factor, such as EF-G), the structure coordinates of the L11/GAR RNA, or portions thereof, as provided by this invention are useful to solve the structure of those other crystal forms of the L11/GAR RNA complex. One method that may be employed for this purpose is molecular replacement. In this method, the unknown crystal structure (i.e., that of the co-complex) may be determined using the L11/GAR complex structure coordinates of this invention as provided in Fig. 7. This method will provide an accurate structural form for the unknown crystal more quickly and efficiently than attempting to determine such information from first principles.

In addition, in accordance with this invention, the L11/GAR complex may be crystallized in co-complex with known GAR inhibitors (e.g., thiostrepton, micrococcin). The crystal structures of such complexes may then be solved by molecular replacement and compared with that of inhibitor-free L11/GAR complex. Critical sites for interaction of the

known inhibitor with the L11/GAR may thus be identified at high resolution. This information provides an additional tool for determining the most efficient binding interactions, for example, increased hydrophobic interactions, between L11/GAR and a chemical entity or compound.

All of the complexes referred to above may be studied using well-known X-ray diffraction techniques and may be refined versus 2-3 Å resolution X-ray data to an R value of about 0.20 or less using computer software, such as X-PLOR (Yale University, ©1992, distributed by Molecular Simulations, Inc.). See, e.g., Blundel & Johnson, *supra*; Methods in Enzymology, 1985, vol. 114 & 115, H. W. Wyckoff et al., eds., Academic Press. The crystallographic information disclosed herein may thus be used to optimize known classes of L11/GAR inhibitors or activators.

Importantly, the X-ray crystal data disclosed herein also allows the design and synthesis of novel classes of L11/GAR inhibitors or activators (i.e., modulators). The design of compounds that bind to or modulate L11/GAR function according to this invention generally involves consideration of several factors. In particular, the compound must be capable of physically and structurally associating with L11/GAR. Non-covalent molecular interactions important in the functional association of L11/GAR with its accessory factors include hydrogen bonding, van der Waals, electrostatic and hydrophobic interactions.

It is recognized that although certain portions of the compound will not directly participate in this association with the L11/GAR, those portions may still influence the overall conformation of the molecule. This, in turn, may have a significant impact on potency. Such conformational requirements include the overall three-dimensional structure and orientation of the chemical entity or compound in relation to all or a portion of the binding site, or the spacing between functional groups of a compound comprising several chemical

entities that directly interact with L11/GAR.

The potential modulating or binding effect of a chemical compound on the L11/GAR may be analyzed prior to its actual synthesis and testing by the use of computer modelling techniques. If the theoretical structure of the given compound suggests insufficient interaction and association between it and the L11/GAR, synthesis and testing of the compound is obviated. However, if computer modelling indicates a strong interaction, the molecule may then be synthesized and tested for its ability to bind to the L11/GAR domain and to inhibit using the assays described herein. In this manner, synthesis of inoperative compounds may be avoided.

A modulating or binding compound of the L11/GAR may be computationally evaluated and designed by means of a series of steps in which chemical entities or fragments are screened and selected for their ability to associate with the individual binding targets on the L11/GAR.

One skilled in the art may use one of several methods to screen chemical entities or fragments for their ability to associate with L11/GAR and more particularly with the individual binding domains comprising the L11/GAR active sites. This process may begin by visual inspection of, for example, the active site on the computer screen based on the L11/GAR RNA coordinates in Fig.7. Selected fragments or chemical entities may then be positioned in a variety of orientations, or "docked", within an individual binding target site of the L11/GAR as defined herein from analysis of the crystal structure data. Docking may be accomplished using software such as Quanta (Molecular Simulations, Inc., San Diego, CA) and Sybyl (Tripos, Inc., St. Louis, MO) followed by energy minimization and molecular dynamics with standard molecular mechanics forcefields, such as CHARMM (Molecular Simulations, Inc., San Diego, CA) and AMBER (University of California at San Francisco).



Specialized computer programs may also assist in the process of selecting fragments or chemical entities. These include:

1. GRID (Goodford, P. J., "A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules", J. Med. Chem., 28, pp. 849-857 (1985)). GRID is available from Oxford University, Oxford, UK.
2. MCSS (Miranker, A. and M. Karplus, "Functionality Maps of Binding Sites: A Multiple Copy Simultaneous Search Method." Proteins: Structure. Function and Genetics, 11, pp. 29-34 (1991)). MCSS is available from Molecular Simulations, San Diego, CA.
3. AUTODOCK (Goodseil, D. S. and A. J. Olsen, "Automated Docking of Substrates to Proteins by Simulated Annealing", Proteins: Structure. Function, and Genetics, 8, pp. 195-202 (1990)). AUTODOCK is available from Scripps Research Institute, La Jolla, CA.
4. DOCK (Kuntz, I. D. et al., "A Geometric Approach to Macromolecule-Ligand Interactions", J. Mol. Biol., 161, pp. 269-288 (1982)). DOCK is available from University of California, San Francisco, CA.
5. CERIOUS II (available from Molecular Simulations, Inc., San Diego, CA).
6. Flexx (Rarey et al., 1996, J. Mol. Biol. 261: 470-489).

Once suitable chemical entities or fragments have been selected, they can be assembled into a single compound or modulator. Assembly may proceed by visual inspection

of the relationship of the fragments to each other on the three-dimensional image displayed on a computer screen in relation to the structure coordinates of the L11/GAR. This would be followed by manual model building using software such as Quanta or Sybyl.

Useful programs to aid one of skill in the art in connecting the individual chemical entities or fragments include:

1. CAVEAT (Bartlett, P. A. et al, "CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules". In "Molecular Recognition in Chemical and Biological Problems", Special Pub., Royal Chem. Soc., 78, pp. 182-196 (1989)). CAVEAT is available from the University of California, Berkeley, CA.
2. 3D Database systems such as MACCS-3D (MDL Information Systems, San Leandro, CA). This area is reviewed in Martin, Y. C., "3D Database Searching in Drug Design", J. Med. Chem., 35, pp. 2145-2154 (1992)).
3. HOOK (available from Molecular Simulations Inc., San Diego, CA.).

Instead of proceeding to build an L11/GAR modulator in a step-wise fashion one fragment or chemical entity at a time as described above, modulatory L11/GAR binding compounds may be designed as a whole or "de novo" using either an empty active site or optionally including some portion(s) of a known inhibitor(s). These methods include:

1. LUDI (Bohm, H.-J., "The Computer Program LUDI: A New Method for the De Novo Design of Enzyme Inhibitors", J. Comp. Aid. Molec. Design, 6, pp. 61-78 (1992)). LUDI is available from Molecular Simulations, Inc., San Diego, CA.

from Molecular Simulations, San Diego, CA.

Other molecular modelling techniques may also be employed in accordance with this invention. See, e.g., Cohen, N. C. et al., "Molecular Modeling Software and Methods for Medicinal Chemistry", J. Med. Chem., 33, pp. 883-894 (1990). See also, Navia, M. A. and M. A. Murcko, "The Use of Structural Information in Drug Design", Current Opinions in Structural Biology, 2, pp. 202-210 (1992); Hubbard, "Can Drugs Be Designed?", Curr. Opin. Biotechnol., 8, pp. 696-700 (1997); and Afshar et al., "Structure-Based and Combinatorial Search for New RNA-Binding Drugs", Curr. Opin. Biotechnol., 10, pp.59-63 (1999).

Once a compound has been designed or selected by the above methods, the efficiency with which that compound may bind to L11/GAR may be tested and optimized by computational evaluation. For example, a compound may be optimized so that in its bound state it would preferably lack repulsive electrostatic interaction with the target site. Such non-complementary (e.g., electrostatic) interactions include repulsive charge-charge, dipole-dipole and charge-dipole interactions. Specifically, the sum of all electrostatic interactions between the modulator and the enzyme when the modulator is bound to L11/GAR preferably make a neutral or favorable contribution to the enthalpy of binding.

Specific computer software is available in the art to evaluate compound deformation energy and electrostatic interaction. Examples of programs designed for such uses include: Gaussian 92, revision C [M. J. Frisch, Gaussian, Inc., Pittsburgh, Pa. ©1992]; AMBER,

version 4.0 [P. A. Kollman, University of California at San Francisco, ©1994];

QUANTA/CHARMM

[Molecular Simulations, Inc., San Diego, CA. ©.1994]; and Insight II/Discover

(Biosym Technologies Inc., San Diego, CA. ©1994). These programs may be implemented,

for instance, using a Silicon Graphics workstation, 02-R10000 or IBM RISC/6000

workstation model 550. Other hardware systems and software packages will be known to

those

skilled in the art.

Once an L11/GAR-binding compound has been optimally selected or designed, as described above, substitutions may then be made in some of its atoms or side groups in order to improve or modify its binding properties. Generally, initial substitutions are conservative, i.e., the replacement group will have approximately the same size, shape, hydrophobicity and charge as the original group. It should, of course, be understood that components known in the art to alter conformation should be avoided. Such substituted chemical compounds may then be analyzed for efficiency of fit to L11/GAR by the same computer methods described in detail, above.

### **Targets for Modification of L11/GAR Function**

The X-ray crystal structure co-ordinates disclosed herein may be used to define structural features of the L11/GAR which represent targets for inhibition or activation of the GTPase activity of the ribosome. The following regions of the L11/GAR, defined by the X-ray co-ordinate data, represent particularly useful targets for the development of inhibitory or activating compounds.

#### **1. L11 N terminus:GAR RNA interface.**

The putative site for binding of the antibiotics thiostrepton and micrococin to the

GAR is between the N terminus of L11 and the interface between the 1067 and 1095 stem loops of the GAR RNA. The structural data as disclosed in Table II and described herein above suggest that the N terminal lobe of L11 behaves as a rigid body that flexes about the so-called “tether sequence” between the C terminal and N terminal lobes of the protein. Therefore, the binding pocket is not limited to those residues at the interface of the L11 N terminus and the GAR RNA that are in direct contact. The binding pocket can include all of the following:

- A) all exposed residues from the L11 N terminus;
- B) all exposed residues from the GAR RNA that are on its L11 binding surface, including A1070, U1061, A1095, A1096, C1097, and A1098;
- C) L11 amino acid residues that are in direct contact with the GAR RNA, including K10, Q12, Q30 and K71;
- D) L11 amino acid residues from the helical region between P20 and H31; and
- E) the L11  $\beta$  sheet between Q8 and P14, and neighboring I53.

Computer simulation techniques may be used to determine which parameters of the binding pocket may be exploited in designing or screening compounds that interact with the binding pocket. Such techniques allow for the construction of structural models that can then be used in designing inhibitory/activating compounds targeted to the L11/GAR binding pocket. These techniques may involve any of the software packages described above or known in the art, and include:

- A) Interactive movement of the L11 N terminus as a rigid body with concurrent geometry optimization, using, for example, Quanta.
- B) Molecular dynamics simulation of the GAR RNA-L11 complex using. For

example, CHARMM and/or AMBER.

C) Normal mode dynamics simulation of the GAR RNA-L11 complex using, for example, CHARMM.

D) Molecular docking of thiostrepton and/or micrococcin to the models of the binding pocket.

## 2. The L11 flexible tether or the flexible tether:GAR RNA interface.

The flexible tether domain of L11 and the GAR RNA surfaces that the tether domain interacts with are defined by the crystal structure coordinates disclosed in Table II and discussed herein above. The X-ray crystal data suggest that the L11 N terminus may act as a molecular switch that triggers the GTPase activity. It is thought that thiostrepton and micrococcin act by modifying the interaction between the L11 N terminus and the GAR RNA. Therefore, the region tethering the N terminal and C terminal lobes of L11, (i.e., amino acids K71 through A75) represent a target for the development of compounds that inhibit or activate GAR function, as does the domain comprising the interface of the tether region with GAR RNA residues. The GAR RNA domain interacting with the tether includes U1061, the backbone of U1060, and G1059. Any molecule that could modify the relative positioning of the L11 NTD and CTD may disrupt the function of the molecular switch and thereby modulate the function of the GAR. For example, this could be performed by a molecule interacting with the L11 tether domain and/or the GAR in close contact with the tether. Any molecule that could interact with both the C terminal and N terminal lobes of L11 and stabilize one orientation of the lobes relative to the alternate orientation may disrupt the function of the molecular switch and thereby disrupt the function of the GAR.

Computer simulation techniques similar to those described above for modeling the

L11 N terminus:GAR RNA interface may be used to determine which parameters of the 4 way junction and  $\text{Cd}^{++}$  coordination site may be exploited in designing or screening compounds that interact with or disrupt the junction/ $\text{Cd}^{++}$  coordination site and/or modify the activity of the GTPase.

### 3. The GAR RNA:EF-G interface.

The interaction of translational elongation factor EF-G with the ribosome has been mapped by directed hydroxyl radical probing (Wilson & Noller, 1998, Cell 92: 131-139). This approach indicated that GAR RNA residues in the region of A1070 and in the region of C1100 are involved in the binding of EF-G. A1070 is included in the GAR RNA:L11 N terminal interface discussed as a target above, but is nonetheless of interest in approaches aimed at disrupting or modifying EF-G binding.

The crystal structure coordinates disclosed in Table II and discussed herein above define the structure of the GAR RNA at C1100, and the RNA bases and L11 amino acid residues around it. This structure defines a novel target for the design and/or selection of molecules that can disrupt the GAR RNA:EF-G interaction.

Computer simulation techniques similar to those described above for modeling the L11 NTD: GAR RNA interface may be used to determine which parameters of the binding pocket may be exploited in designing or screening compounds that modify the relative positioning of L11 NTD and CTD and modify the activity of the GTPase.

### 4. RNA Folding/Stability.

The X-ray crystal structure coordinates disclosed in Table II and discussed herein above define the structure of a novel "4 way junction" fold in the ribosomal RNA in the L11/GARcomplex. The data further reveal the importance of a  $\text{Cd}^{++}$  ion that occupies the center of the four way junction between bases 1056-1057 and 1086-1087. Because a ligand

that can modify the folding of the RNA would be predicted to disrupt or otherwise modify the GTPase activity, this folded RNA structure represents a strong target for development of inhibitors or activators of the GTPase. Because the  $\text{Cd}^{++}$  ion likely stabilizes the unusual RNA fold, the region defined by those amino acid and RNA residues interacting with the  $\text{Cd}^{++}$  ion is particularly attractive as a target.

### **5. The L11 C terminus:GAR RNA interface.**

The domain comprising the interaction surface of the C terminal lobe of L11 and the GAR RNA is defined by the crystal structure data disclosed in Table II (X-ray co-ord's) and is described herein above. The crystal data indicate that the C terminus of L11 interacts very tightly with the GAR RNA. As such, the interaction may be difficult to disrupt. Computer simulation techniques similar to those described above for modeling the L11 N terminus:GAR RNA interface may be used to determine which parameters of the binding pocket may be exploited in designing or screening compounds that interact with the C terminal L11: GAR RNA interface domain and/or modify the activity of the GTPase.

The analysis of the various targets made possible by the crystal structure coordinate data disclosed herein, including the GAR RNA:L11 interface, the GAR RNA:L11: Micrococccin interface, the L11 N terminus:L11 C terminus interface (with or without GAR RNA), the GAR RNA:EF-G interface, and the GAR RNA:L11:EF-G interface, may be used to define specific features (e.g., a pattern of hydrogen bond donors and acceptors, a hydrophobic patch, etc.) of these targets. These features in turn define a three dimensional "pharmacophore" pattern. This pattern can then be used to screen virtual libraries of existing compounds, such as the Available Chemical Directory (MDL, Inc.) for compounds exhibiting the desired combination of chemical entities. In this screening, the quality of fit of such entities or compounds to the target site may be judged by a scoring fuction. The scoring



function can account for shape complementarity (Katchalski-Katzir et al., 1992, Proc. Natl. Acad. Sci. USA, 89, pp.2195-2199.), estimated interaction energy (Meng et al., 1992, J.Comp. Chem., 13, pp. 505-524), surface accessibility, or a combination of these (see for example, Bohm, 1994, J. Comp. Aided Mol. Design, pp.243-256). A program such as Catalyst (MSI) can perform this task. Libraries of compounds can also be screened virtually using the coordinates of the targets and molecular docking programs such as DOCK (UCSF) or FLEXX.

Once one or more compounds have been identified as potential ligands using any of the methods described above, they may be screened for biological activity.

A variety of assays can be used to evaluate the activity of compounds designed to inhibit the activity of the L11/GAR. These include, but are not limited to: inhibition of bacterial growth, inhibition of in vitro protein synthesis using messenger RNA as a template, inhibition of the elongation phase of in vitro protein synthesis using polyU as a template, inhibition of GTP hydrolysis mediated by EF-G as described by Pestka (1970) and Rodnina et al. (1997); activation of GTP hydrolysis mediated by EF-G as described by Cundliffe and Thompson (1981). Binding of EF-G to both the L11/GAR complex and to the sarcin/ricin domain can be measured as described by Munishkin and Wool (1997, Proc. Natl. Acad. Sci. USA 94, 12280-12284; "The ribosome in pieces: Binding of elongation factor EF-G to oligoribonucleotides that mimic the sarcin/ricin and thiostrepton domains of 23S ribosomal RNA").

In addition, compound interaction with the L11/GAR complex can be evaluated by direct binding assays. Filter binding assays that measure the ability of thiostrepton to cause retention of radiolabelled GAR RNA to nitrocellulose filters have been described by

GuhaThakurta and Draper (1999; Biochemistry, 38, 3633-3640 "Protein-RNA sequence covariation in a ribosomal protein-rRNA complex"). As revealed herein, these assays can be modified to evaluate small molecules that competitively inhibit the binding of thiostrepton and/or micrococccin to the L11/GAR complex or to GAR. For molecules that do not themselves cause filter retention, the RNA may be labelled. For molecules that do cause filter retention, the RNA and/ or RNA-protein complex can be immobilised on a solid support and the binding of radiolabelled thiostrepton or other known L11/GAR binding compound can be measured. Thiostrepton or micrococccin can be labelled metabolically by incorporation of <sup>35</sup>S, <sup>3</sup>H or <sup>14</sup>C labelled precursors, or post-synthetically by modification of the molecule with radiolabllled precursors. In addition thiostrepton or micrococccin can be labelled with another detectable group, including, but not limited to, fluorescent and luminescent groups.

Displacement assays can also be performed by using as reporter molecules any labelled molecule that binds to the L11/GAR complex or GAR RNA with an affinity of 50 uM or less. Suitable reporters include, but are not limited to, oligonucleotides, peptides and oligonucleotide-peptide conjugates.

#### **Libraries for Screening According to the Invention.**

Inhibitors and/or activators identified according to the methods of the invention may be provided from libraries of compounds available from a number of sources or may be derived by combinatorial chemistry approaches known in the art. Such libraries include but are not limited to the available Chemical Directory, Maybridge, and natural product collections.

Compounds identified as ligands using the methods described herein may be further optimized to improve binding activity. Using the docked models of the known ligands

thiostrepton and micrococcin, it is possible to identify structures of the ligand that may be altered to improve binding affinity. Similarly, features of a ligand that are identified as unimportant for binding may be excluded to reduce the molecular weight of the ligand.

## EXAMPLES

In order that the invention described herein may be more fully understood, the following examples are set forth. It should be understood that these examples are for illustrative purposes only and are not to be construed as limiting this invention in any manner.

### EXAMPLE 1: Preparation and Analysis of L11/GAR RNA Crystal.

#### A. Sample Preparation

The gene for *T. maritima* ribosomal protein L11 was cloned and overexpressed in *E. coli* using the T7-based expression system (Studier et al., 1990). The protein was purified by a combination of cation-exchange, hydroxylapatite and size-exclusion chromatography as reported for the purification of ribosomal protein S7 (Wimberly et al., 1997). For cocrystallization with RNA, the protein was dialysed into a buffer A containing 0.1 M KCl, 5 mM Na-cacodylate pH 6.0, 0.1 mM Na<sub>2</sub>EDTA, 1 mM DTT. A fragment of RNA corresponding to nucleotides 1111-1168 of *T. maritima* 23S rRNA was synthesized by *in vitro* run-off transcription from a linearized plasmid using T7 RNA polymerase. The plasmid contained the following elements: a T7 promoter, a self-cleaving hammerhead ribozyme to generate a homogeneous RNA 5' end (Price et al., 1995), a template for the target RNA sequence, and a Pst I site used for plasmid linearization. RNA was purified on denaturing polyacrylamide slab gels, eluted, concentrated by ethanol precipitation, and dialyzed into

buffer A. The RNA was reannealed by heating to 90 °C and slow cooling. L11 protein was added to yield a 1:1 RNA:protein mixture, which was concentrated to 0.15 mM in each component for crystallization experiments.

## B. Crystallization and Structure Determination

Crystals of the complex were obtained at 4 °C using the hanging drop technique. The equimolar mixture of L11 and RNA in dialysis buffer A was mixed with an equal volume of well solution (25% glycerol, 15% PEG 4000, 0.2 M KCl, 50 mM MgCl<sub>2</sub>, 20 mM CdCl<sub>2</sub>, 1 mM DTT, 50 mM Tris pH 7.5 at 22 °C). The crystals were in the space group P2<sub>1</sub>2<sub>1</sub>2<sub>1</sub>, with cell dimensions of  $a = 63.9 \text{ \AA}$ ,  $b = 84.3 \text{ \AA}$  and  $c = 155.5 \text{ \AA}$ , and diffracted to better than 2.6 Å resolution using a synchrotron source. Diffraction data were collected under cryogenic conditions, and the crystals were flash-frozen by plunging into liquid nitrogen. For mercury derivatization, crystals were soaked for 24 hours in the well solution containing 1 mM CH<sub>3</sub>HgNO<sub>3</sub> but lacking DTT. Efforts to obtain cocrystals of RNA with selenomethionine-substituted L11 were unsuccessful, apparently because the preparation of selenomethionyl L11 used was at least partly misfolded.

The structure was solved using a multiwavelength anomalous diffraction (MAD) experiment (Hendrickson, 1991) on the methylmercury derivative. Straightforward isomorphous replacement was not possible because the derivative is not isomorphous with native crystals. Because the mercury LIII edge does not have a significant white line, data were collected at just two wavelengths, the inflection point of the mercury edge at 1.01 Å and a remote wavelength at 0.98 Å. This remote wavelength is near the maximum  $f''$  for accurate measurement of anomalous differences, and is also sufficiently remote from the inflection point to give useful isomorphous differences. Data were collected from a single flash-cooled

crystal at beamline X12-C of the NSLS. To optimize measurement of anomalous differences, we used the inverse beam method in which pairs of sweeps separated by 180 degrees in were collected every 30 degrees. The data were integrated and scaled using the HKL suite of programs (Otwinowski and Minor, 1997).

Phasing was done by treating MAD as a special case of MIR (Ramakrishnan and Biou, 1997; Ramakrishnan et al., 1993). Local scaling of the data, determination of initial heavy atom sites, and initial phasing was done using the program SOLVE (Terwilliger and Berendzen, 1999). Subsequent phasing was done using the program SHARP (de la Fortelle and Bricogne, 1997). A significant improvement in phasing was obtained by including several well-ordered cadmium sites in a final round of SHARP heavy atom refinement. Each round of phasing was followed by density modification with Solomon (Abrahams and Leslie, 1996). The unaveraged, solvent-flattened map revealed virtually unbroken main-chain density for the RNA and the L11 C-terminal domains of both complexes in the asymmetric unit, which were easily built using the program O (Jones and Kjeldgaard, 1997). Twofold non-crystallographic symmetry (NCS) averaging followed by solvent flattening was then carried out using NCS and solvent masks based on the RNA and C-terminal domain coordinates. The resulting map was of high quality and revealed a few minor building errors, but the L11 N-terminal domain density was still of insufficient quality to permit unambiguous fitting. Interpretation of the density for the entire L11 N-terminal domain was possible only from iterative rounds of refinement and  $2F_o - F_c$  maps. The final model was refined to an Rfree of 27 % using the program X-PLOR (Brünger, 1988) using standard parameters for protein (Engh and Huber, 1991) and nucleic acid (Parkinson et al., 1996) structure refinement. Magnesium and cadmium ions were distinguished by inspection of an anomalous difference Fourier map.

Magnesium ions were distinguished from ordered waters by inspection of  $2F_o - F_c$  maps, in which an octahedral coordination of magnesium by water and RNA ligands was often visible. A Ramachandran plot of the protein revealed only three outliers, Lys93 in the C-terminal domain, which clearly has a positive phi angle in the original experimental map, and Ala21 and Val24 in the N-terminal domain, for which the side chains are very poorly defined. Details of the data collection, phasing and refinement are shown in Table I.

**EXAMPLE 2. Use of the Ribosomal Protein L11/GAR Crystal Structure Coordinates to Design a Modulator of GAR Activity.**

Example 1 illustrates the methods involved in generating a structure of the L11/GAR RNA complex at atomic resolution. The crystal structure data make clear, for example, that the N terminus of L11 can move within the context of the L11/GAR. Because the crystal structure data, in conjunction with available biochemical data, point to a molecular switch mechanism whereby the relative position of the L11 N terminal lobe determines the activity of the GAR, it is of interest to select or design compounds that can effect restriction of modification of this movement.

1. Modeling the movement and interactions of the L11 N terminal lobe.

One of skill in the art may use the crystal structure coordinates, along with the software package Quanta to interactively model the movement of the L11 N terminus as a rigid body relative to the other GAR surfaces. This model will provide information on the many possible interactions between the L11 N terminus and the other amino acid and nucleotide residues comprising the GAR, as well as solvent interactions.

To develop a more detailed picture of the molecular interactions involving the L11 N terminal lobe in the GAR, the software packages CHARMM and AMBER may be applied by one of skill in the art to the crystal structure coordinates. These will provide a molecular

dynamics simulation of the N terminal lobe of L11 within the L11/ GAR RNA complex.

Similarly, CHARMM may be used by one of skill in the art to provide a normal mode dynamics simulation of the L11 N terminal lobe within the L11/GAR context.

Finally, the crystal structure coordinates allow the use of software packages such as DOCK or to simulate docking of the known GAR modulators thiostrepton and micrococin with the GAR, thereby providing a finely detailed description of those interactions within the GAR critical to its function.

Used in combination, the software approaches described above can manipulate the crystal structure coordinate data to provide a very high resolution three dimensional model of the L11 N terminal lobe and its interactions with other portions of the GAR including van der Waals contacts, electrostatic interactions and hydrogen bonding opportunities.

## 2. Design of a candidate modulator compound.

Once a detailed three dimensional model of the L11/GAR has been created as described above, one of skill in the art may use the grid-based software approaches GRID or CERIUS II, and MCSS techniques (see, for example, Castro et al., 1999, Medicinal Chem. Res. 9: 98-107) to map favorable interaction positions for functional groups such as protons, hydroxyl groups, amine groups, divalent cations, aromatic and aliphatic functional groups, acetamide, methanol, etc. Once a set of favorable groups for each position are predicted, one of skill in the art may take one of two different approaches to designing a modulator.

First, one may assemble the moieties predicted to interact with the various critical parts of the L11/GAR surfaces into a single molecule. This may be accomplished by one of skill in the art using the software packages CAVEAT, MACCS-3D or HOOK. One of skill in the art may then synthesize the selected compounds for in vitro and in vivo testing for effects on GAR activity.

Alternatively, one may screen a database, such as the MDL Available Chemical Directory to potentially find existing compounds that combine the required moieties in a favorable conformation for GAR binding. The software packages Catalyst, DOCK and FLEXX may be used to advantage for this purpose by one of skill in the art.

### **EXAMPLE 3. Assaying the Activity of a Candidate Modulator by Displacement of Thiostrepton from the GAR**

Thiostrepton binding to GTPase centre RNA can be monitored by a filter binding assays (Uchiumi et al., 1995, Biol. Chem., 270(50):29889-93; Draper et al., 1988, Methods Enzymol., 164:203-20). The filter binding assay can be transformed to a 96-well format using Millipore MHAB (mixed cellulose ester) 96-well plates. The dissociation constant for the thiostrepton/GTPase centre-59mer complex of 1uM is in good accordance with the literature. Additionally, filter binding can show the cooperativity in binding of thiostrepton and L11. *Thermotoga maritima* ribosomes are known to be sensitive to thiostrepton (Londei et al., 1988, J. Bacteriol., 170(9):4353-60), although 100-fold less than *B. stearothermophilus* ribosomes. The affinity of thiostrepton for *Thermotoga* GTPase center RNA in vitro has not yet been determined.

<sup>35</sup>S- or <sup>32</sup>P-labelled RNA is prepared by transcription in the presence of radiolabelled nucleotides. The labelled RNAs are purified by gel electrophoresis or chromatography by reverse-phase. For filter binding assays the RNA are renatured and 3,000 to 10,000 cpm of RNA are used per assay. Association constants between RNA and thiostrepton in the presence or absence of inhibitor are determined in 100 ul reactions containing 10 mM Tris-HCl (pH 7.4), 3 mM MgCl<sub>2</sub>, 175 mM NH<sub>4</sub>Cl and 5% v/v DMSO. The reaction mixtures also contain between 2 and 10 uM thiostrepton and a range of inhibitor



concentrations up to 50  $\mu$ M. The RNA-thiostrepton-inhibitor mixtures are incubated for 15 min at room temperature (approximately 22°C) prior to filtration through the nitrocellulose filter membranes.

For high-throughput screening, the assay can be performed in 96-well filter plates (Multiscreen HA filtration plates, Millipore) with nitrocellulose membranes incorporated into the bottom of each well and filtered using Multiscreen vacuum Manifold ( Millipore). The filters are washed once with 100  $\mu$ l buffer before determining their radioactivities using Microbeta Liquid Scintillation Counter (Wallac).

The relative amounts of RNA retained in the presence and absence of inhibitor can be determined by quantitation of the radioactivity on each filter. Compounds that reduce the amount of RNA retained on the filter in a concentration dependent manner are competitive inhibitors of thiostrepton binding to the RNA.

#### **EXAMPLE 4. Binding assays with radioactive thiostrepton**

Binding of [ $^{35}$ S]-labelled thiostrepton to 23S RNA and ribosomes has been shown by gel filtration of RNA and RNA/L11 complexes together with thiostrepton as well as by charcoal (Norit) absorption of unbound [ $^{35}$ S]thiostrepton (Thompson et al., 1979. Eur. J. Biochem., 98(1):261-5). Using equilibrium dialysis, the dissociation constant of thiostrepton/23S RNA has been determined as 0.23 $\mu$ M (Thompson & Cundliffe, 1991, Biochimie 1991, 73(7-8):1131-5). The affinity to intact ribosomes is 100-1000fold higher (Pestka et al., 1976, Anal. Biochem., 71(1):137-42).

The ability of biotinylated GTPase centre-59mer to bind thiostrepton (as shown by filter binding) gives a route for a displacement assay employing displacement of

[<sup>3</sup>H]-labelled thiostrepton (Amersham) from an immobilised GTPase centre RNA/L11 complex or from ribosomes.

#### **EXAMPLE 5. Luciferase translation assay**

Using an *E. coli* S30 lysate and luciferase mRNA (Promega *E. coli* S30 extract system for linear templates; Cat No: L1030) the active luciferase protein can be synthesised *in vitro* and the relative amount of luciferase generated is monitored in a bioluminescence assay. The mRNA is either provided by coupled transcription/translation using the linearized plasmid pBESTLucTM as a template or by adding purified luciferase mRNA.

The addition of ribosome-inactivating compounds or antibiotics directed to protein biosynthesis (thiostrepton, kanamycin, chloramphenicol and others) leads to a decrease in yield of active luciferase compared to the control. Compound and antibiotic titrations can be used to determine IC<sub>50</sub> values (see Langer et al., 1996, *Anal. Biochem.*, 243(1):150-3).

#### **EXAMPLE 6. Additional translation assays**

An S30 transcription/translation system (Promega) can be used to incorporate [<sup>35</sup>S]methionine into protein translated from MS2 phage RNA. Translation yield is quantified after alkaline hydrolysis by acid precipitation of the synthesised peptides and scintillation counting. Whole-cell protein synthesis can be measured adding [<sup>14</sup>C]leucine to exponentially growing *E. coli* cells and measuring the incorporation into protein by alkaline hydrolysis and TCA precipitation (see Shinabarger et al., 1997, *Antimicrob. Agents Chemother.*, 41(10):2132-6).

**EXAMPLE 7. Assay of Translation Elongation**

Translation elongation is measured using isolated polysomes from *E. coli* MRE600 (Girbes et al., 1979, *Methods Enzymol.*, 59:353-62), S100 extract from *E. coli* and poly(U) (Sigma) as a template (e.g. Grise-Miron et al., 1981, *Biochim. Biophys. Acta*, 656(1):103-10). Incorporation of [<sup>3</sup>H]phenylalanine into polyphenylalanine is quantified by acid precipitation and scintillation counting.

**EXAMPLE 8. In vitro EF-G-dependent GTP Hydrolysis**

Thiostrepton acts on the tRNA translocation step of translation elongation and inhibits elongation factor G (EF-G)-dependent GTP hydrolysis (Pestka et al., 1970, *Biochem. Biophys. Res. Commun.*, 40(3):667-74; Rodnina et al., 1997, *Nature*, 385:37-41). EF-G is known to contact the GTPase centre region of 23S RNA (Skold et al., 1983, *Nucleic Acids Res.*, 11(14):4923-32; Moazed & Noller, 1986, *Nature*, 334:362-4). 70S ribosomes support GTP hydrolysis by EF-G in the absence of other factors normally necessary for protein synthesis. Uncoupled GTP hydrolysis and the inhibition by thiostrepton or other compounds can be measured in an assay containing purified ribosomes, purified EF-G and gamma-[<sup>32</sup>P]-GTP (Stark&Cundliffe, 1979, *J. Mol. Biol.*, 134(4):767-9; Lill et al., 1988, *EMBO J.*, 8(12):3933-8).

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**Table I**  
Crystallographic statistics

<u>Data collection</u>	<u><math>\lambda 1</math> (1.008 Å)</u>	<u><math>\lambda 2</math> (0.980 Å)</u>
Reflections	104,096	107,907
Independent reflections	25,927	25,894
Completeness	99% (98%)*	98% (97%)*
Mean ( $I$ / sigma ( $I$ ))	20 (4.2)*	20 (4.5)*
$R_{\text{sym}}$	4.1% (17%)*	4.2% (17%)*
$d_{\text{min}}$ (Å)	2.6	2.6
$f'$ (Hg) (electrons)**	-12.0	-9.0
$f''$ (Hg) (electrons)**	6.4	8.0
$f'$ (Cd) (electrons)**	-0.42	-0.46
$f''$ (Cd) (electrons)**	2.3	2.2

\*Values in parentheses refer to the highest resolution shell.

\*\*Values after SHARP refinement.

<u>Phasing</u>	<u><math>\lambda 1</math>-<math>\lambda 2</math> isomorphous</u>	<u><math>\lambda 1</math> anomalous</u>	<u><math>\lambda 2</math></u>
<u>anomalous</u>			
$R_{\text{Cullis}}$ (centrics)	0.50	--	--
$R_{\text{Kraut}}$ (acentrics)	0.09	0.025	0.023
Phasing power (acentrics)	1.25	1.54	1.52

Mean figure of merit (acentrics) 0.39

Mean figure of merit (centrics) 0.23

### Refinement

Number of atoms 4196 (2474 RNA, 1524 protein, 198 water & ions)

$R_{\text{cryst}} / R_{\text{free}}$  (5% of data) 0.228 / 0.253

RMS deviation from ideal geometry

bond lengths 0.005 Å

bond angles 1.2 degrees

COMPND MOL\_ID: 1;  
COMPND 2 MOLECULE: 23S RIBOSOMAL RNA;  
COMPND 3 CHAIN: C, D;  
COMPND 4 FRAGMENT: FRAGMENT 1051-1108;  
COMPND 5 MUTATION: U1108C;  
COMPND 6 OTHER\_DETAILS: COVALENT MERCURY LIGAND AT U1061;  
COMPND 7 MOL\_ID: 2;  
COMPND 8 MOLECULE: RIBOSOMAL PROTEIN L11;  
COMPND 9 CHAIN: A, B;  
COMPND 10 ENGINEERED: YES;  
COMPND 11 OTHER\_DETAILS: COVALENT MERCURY LIGAND AT CYS39

SOURCE 1 MOL\_ID: 1;  
SOURCE 2 ORGANISM\_SCIENTIFIC: THERMOTOGA MARITIMA;  
SOURCE 3 OTHER\_DETAILS: IN VITRO TRANSCRIBED RNA;  
SOURCE 4 MOL\_ID: 2;  
SOURCE 5 ORGANISM\_SCIENTIFIC: THERMOTOGA MARITIMA;  
SOURCE 6 EXPRESSION\_SYSTEM: ESCHERICHIA COLI;  
SOURCE 7 EXPRESSION\_SYSTEM\_STRAIN: BL21(DE3);  
SOURCE 8 EXPRESSION\_SYSTEM\_PLASMID: PET13A;  
SOURCE 9 OTHER\_DETAILS: RECOMBINANT PROTEIN  
KEYWDS RNA-PROTEIN COMPLEX, RNA, RIBOSOME, TRANSLOCATION,  
  
KEYWDS 2 THIOSTREPTON  
EXPDTA X-RAY DIFFRACTION  
AUTHOR B.T.WIMBERLY,R.GUYMON,J.P.MCCUTCHEON,S.W.WHITE,  
AUTHOR 2 V.RAMAKRISHNAN  
REMARK 1  
REMARK 1 REFERENCE 1  
REMARK 1 AUTH Y.XING,D.DRAPER  
REMARK 1 TITL COOPERATIVE INTERACTIONS OF RNA AND THIOSTREPTON  
  
REMARK 1 TITL 2 ANTIBIOTIC WITH TWO DOMAINS OF RIBOSOMAL PROTEIN  
  
REMARK 1 TITL 3 L11  
REMARK 1 REF BIOCHEMISTRY V. 35 1581 1996  
REMARK 1 REFN ASTM BICHAW US ISSN 0006-2960 0033  
REMARK 1 REFERENCE 2  
REMARK 1 AUTH J.THOMPSON,F.SCHMIDT,E.CUNDLIFFE

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REMARK 1 TITL SITE OF ACTION OF A RIBOSOMAL RNA METHYLASE
REMARK 1 TITL 2 CONFERRING RESISTANCE TO THIOSTREPTON
REMARK 1 REF J.BIOL.CHEM. V. 257 7915 1982
REMARK 1 REFN ASTM JBCHA3 US ISSN 0021-9258 0071
REMARK 1 REFERENCE 3
REMARK 1 AUTH J.THOMPSON,E.CUNDLIFFE,M.STARK
REMARK 1 TITL BINDING OF THIOSTREPTON TO A COMPLEX OF 23S RNA
REMARK 1 TITL 2 WITH RIBOSOMAL PROTEIN L11
REMARK 1 REF EUR.J.BIOCHEM. V. 98 261 1979
REMARK 1 REFN ASTM EJBCAI IX ISSN 0014-2956 0262
REMARK 2
REMARK 2 RESOLUTION. 2.57 ANGSTROMS.
REMARK 3
REMARK 3 REFINEMENT.
REMARK 3 PROGRAM : X-PLOR 3.851
REMARK 3 AUTHORS : BRUNGER
REMARK 3
REMARK 3 DATA USED IN REFINEMENT.
REMARK 3 RESOLUTION RANGE HIGH (ANGSTROMS) : 2.57
REMARK 3 RESOLUTION RANGE LOW (ANGSTROMS) : 20.0
REMARK 3 DATA CUTOFF (SIGMA(F)) : 0.0
REMARK 3 DATA CUTOFF HIGH (ABS(F)) : 1000000.0
REMARK 3 DATA CUTOFF LOW (ABS(F)) : 0.001
REMARK 3 COMPLETENESS (WORKING+TEST) (%) : 95.5
REMARK 3 NUMBER OF REFLECTIONS : 49313
REMARK 3
REMARK 3 FIT TO DATA USED IN REFINEMENT.
REMARK 3 CROSS-VALIDATION METHOD : THROUGHOUT
REMARK 3 FREE R VALUE TEST SET SELECTION : RANDOM
REMARK 3 R VALUE (WORKING SET) : 0.219
REMARK 3 FREE R VALUE : 0.254
REMARK 3 FREE R VALUE TEST SET SIZE (%) : 4.9
REMARK 3 FREE R VALUE TEST SET COUNT : 2398
REMARK 3 ESTIMATED ERROR OF FREE R VALUE : 0.005
REMARK 3
REMARK 3 FIT IN THE HIGHEST RESOLUTION BIN.
REMARK 3 TOTAL NUMBER OF BINS USED : 6
REMARK 3 BIN RESOLUTION RANGE HIGH (A) : 2.57
REMARK 3 BIN RESOLUTION RANGE LOW (A) : 2.73
REMARK 3 BIN COMPLETENESS (WORKING+TEST) (%) : 86.2
REMARK 3 REFLECTIONS IN BIN (WORKING SET) : 7101
REMARK 3 BIN R VALUE (WORKING SET) : 0.386
REMARK 3 BIN FREE R VALUE : 0.432
REMARK 3 BIN FREE R VALUE TEST SET SIZE (%) : 4.5
REMARK 3 BIN FREE R VALUE TEST SET COUNT : 331

```



REMARK 3 ESTIMATED ERROR OF BIN FREE R VALUE : 0.024  
 REMARK 3  
 REMARK 3 NUMBER OF NON-HYDROGEN ATOMS USED IN REFINEMENT.  
  
 REMARK 3 PROTEIN ATOMS : 1524  
 REMARK 3 NUCLEIC ACID ATOMS : 2474  
 REMARK 3 HETEROGEN ATOMS : 35  
 REMARK 3 SOLVENT ATOMS : 142  
 REMARK 3  
 REMARK 3 B VALUES.  
 REMARK 3 FROM WILSON PLOT (A\*\*2) : 58.8  
 REMARK 3 MEAN B VALUE (OVERALL, A\*\*2) : 42.8  
 REMARK 3 OVERALL ANISOTROPIC B VALUE.  
 REMARK 3 B11 (A\*\*2) : NULL  
 REMARK 3 B22 (A\*\*2) : NULL  
 REMARK 3 B33 (A\*\*2) : NULL  
 REMARK 3 B12 (A\*\*2) : NULL  
 REMARK 3 B13 (A\*\*2) : NULL  
 REMARK 3 B23 (A\*\*2) : NULL  
 REMARK 3  
 REMARK 3 ESTIMATED COORDINATE ERROR.  
 REMARK 3 ESD FROM LUZZATI PLOT (A) : 0.32  
 REMARK 3 ESD FROM SIGMAA (A) : 0.45  
 REMARK 3 LOW RESOLUTION CUTOFF (A) : 5.00  
 REMARK 3  
 REMARK 3 CROSS-VALIDATED ESTIMATED COORDINATE ERROR.  
 REMARK 3 ESD FROM C-V LUZZATI PLOT (A) : 0.39  
 REMARK 3 ESD FROM C-V SIGMAA (A) : 0.50  
 REMARK 3  
 REMARK 3 RMS DEVIATIONS FROM IDEAL VALUES.  
 REMARK 3 BOND LENGTHS (A) : 0.005  
 REMARK 3 BOND ANGLES (DEGREES) : 1.0  
 REMARK 3 DIHEDRAL ANGLES (DEGREES) : 28.8  
 REMARK 3 IMPROPER ANGLES (DEGREES) : 1.40  
 REMARK 3  
 REMARK 3 ISOTROPIC THERMAL MODEL : RESTRAINED  
 REMARK 3  
 REMARK 3 ISOTROPIC THERMAL FACTOR RESTRAINTS. RMS SIGMA  
 REMARK 3 MAIN-CHAIN BOND (A\*\*2) : 3.59 ; 1.50  
 REMARK 3 MAIN-CHAIN ANGLE (A\*\*2) : 5.28 ; 2.00  
 REMARK 3 SIDE-CHAIN BOND (A\*\*2) : 6.59 ; 2.00  
 REMARK 3 SIDE-CHAIN ANGLE (A\*\*2) : 9.24 ; 2.50  
 REMARK 3  
 REMARK 3 NCS MODEL : RESTRAINTS  
 REMARK 3

REMARK 3 NCS RESTRAINTS. RMS SIGMA/WEIGHT  
 REMARK 3 GROUP 1 POSITIONAL (A): 0.07 ; 50  
 REMARK 3 GROUP 1 B-FACTOR (A\*\*2): 5.51 ; 2  
 REMARK 3 GROUP 2 POSITIONAL (A): 0.07 ; 50  
 REMARK 3 GROUP 2 B-FACTOR (A\*\*2): 5.51 ; 2  
 REMARK 3  
 REMARK 3 PARAMETER FILE 1 : DNA-RNA-MULTI-ENDO.PARAM  
 REMARK 3 PARAMETER FILE 2 : PROTEIN\_REP.PARAM  
 REMARK 3 TOPOLOGY FILE 1 : DNA-RNA-MULTI-ENDO.TOP  
 REMARK 3 TOPOLOGY FILE 2 : TOPHCSDX.PRO  
 REMARK 3 TOPOLOGY FILE 3 : TOPH19.SOL  
 REMARK 3  
 REMARK 3 OTHER REFINEMENT REMARKS: NCS RESTRAINTS APPLIED TO RNA  
 REMARK 3 THROUGHOUT, NOT TO PROTEIN  
 REMARK 5  
 REMARK 5 WARNING  
 REMARK 5 : THIS IS LAYER 1 RELEASE.  
 REMARK 5  
 REMARK 5 PLEASE NOTE THAT THIS ENTRY WAS RELEASED AFTER DEPOSITOR  
 REMARK 5 CHECKING AND APPROVAL BUT WITHOUT PDB STAFF  
 INTERVENTION.  
 REMARK 5 AN AUXILIARY FILE, AUX .RPT, IS AVAILABLE FROM THE  
 REMARK 5 PDB FTP SERVER AND IS ACCESSIBLE THROUGH THE 3DB BROWSER.  
 REMARK 5 THE FILE CONTAINS THE OUTPUT OF THE PROGRAM WHAT\_CHECK  
 AND  
 REMARK 5 OTHER DIAGNOSTICS.  
 REMARK 5  
 REMARK 5 NOMENCLATURE IN THIS ENTRY, INCLUDING HET RESIDUE NAMES  
 REMARK 5 AND HET ATOM NAMES, HAS NOT BEEN STANDARDIZED BY THE PDB  
 REMARK 5 PROCESSING STAFF. A LAYER 2 ENTRY WILL BE RELEASED SHORTLY  
 REMARK 5 AFTER THIS STANDARDIZATION IS COMPLETED AND APPROVED BY  
 THE  
 REMARK 5 DEPOSITOR. THE LAYER 2 ENTRY WILL BE TREATED AS A  
 REMARK 5 CORRECTION TO THIS ONE, WITH THE APPROPRIATE REVDAT  
 RECORD.  
 REMARK 5  
 REMARK 5 FURTHER INFORMATION INCLUDING VALIDATION CRITERIA USED IN  
 REMARK 5 CHECKING THIS ENTRY AND A LIST OF MANDATORY DATA FIELDS  
 REMARK 5 ARE AVAILABLE FROM THE PDB WEB SITE AT  
 REMARK 5 [HTTP://WWW.PDB.BNL.GOV/](http://www.pdb.bnl.gov/).  
 REMARK 6  
 REMARK 6 THE ASYMMETRIC UNIT CONTAINS TWO L11-RNA COMPLEXES.  
 COMPLEX  
 REMARK 6 1 CONSISTS OF CHAINS A AND C, AND COMPLEX 2 CONSISTS OF

PDB-50000000

REMARK 6 CHAINS B AAND D. RESIDUES 1-7 AND 141 OF CHAIN A ARE  
 REMARK 6 DISORDERED. THE DENSITY FOR RESIDUES 8-70 OF CHAIN A WAS OF  
 REMARK 6 SIGNIFICANTLY LOWER QUALITY THAN THE DENSITY FOR THE  
 REMARK 6 REMAINDER OF THE ASYMMETRIC UNIT, AND THE QUALITY OF THE  
 REMARK 6 MODEL FOR THIS N-TERMINAL DOMAIN IS LOWER THAN THAT OF  
 THE  
 REMARK 6 C-TERMINAL DOMAIN (RESIDUES 71-140). RESIDUES 1-70 AND 141  
 REMARK 6 OF CHAIN B ARE DISORDERED. THE RNA IS NUMBERED WITH THE E.  
 REMARK 6 COLI NUMBERING TO FACILITATE COMPARISON WITH THE  
 EXTENSIVE  
 REMARK 6 BIOCHEMICAL DATA ON THE E. COLI RNA-L11 SYSTEM. THE E. COLI  
 REMARK 6 RNA NUMBERING IS ALSO USED IN THE PRIMARY REFERENCE  
 REMARK 6 DESCRIBING THIS STRUCTURE.  
 REMARK 7 ...  
 REMARK 7 TER  
 REMARK 7 ASP: TERMINAL RESIDUE NOT SEEN IN MAPS  
 REMARK 7 ASP: TERMINAL RESIDUE NOT SEEN IN MAPS  
 REMARK 200  
 REMARK 200 EXPERIMENTAL DETAILS  
 REMARK 200 EXPERIMENT TYPE : X-RAY DIFFRACTION  
 REMARK 200 DATE OF DATA COLLECTION : 24-SEP-1998  
 REMARK 200 TEMPERATURE (KELVIN) : 100  
 REMARK 200 PH : 8.3  
 REMARK 200 NUMBER OF CRYSTALS USED : 1  
 REMARK 200  
 REMARK 200 SYNCHROTRON (Y/N) : Y  
 REMARK 200 RADIATION SOURCE : NSLS  
 REMARK 200 BEAMLINE : X12C  
 REMARK 200 X-RAY GENERATOR MODEL : NULL  
 REMARK 200 MONOCHROMATIC OR LAUE (M/L) : M  
 REMARK 200 WAVELENGTH OR RANGE (A) : 0.98,1.01  
 REMARK 200 MONOCHROMATOR : SI CRYSTAL  
 REMARK 200 OPTICS : MIRRORS  
 REMARK 200  
 REMARK 200 DETECTOR TYPE : BRANDEIS 1K X 1 K CCD  
 REMARK 200 DETECTOR MANUFACTURER : NULL  
 REMARK 200 INTENSITY-INTEGRATION SOFTWARE : DENZO  
 REMARK 200 DATA SCALING SOFTWARE : SCALEPACK

0099305 4400  
 101011 5036660

```

REMARK 200
REMARK 200 NUMBER OF UNIQUE REFLECTIONS : 49313
REMARK 200 RESOLUTION RANGE HIGH (A) : 2.57
REMARK 200 RESOLUTION RANGE LOW (A) : 20.0
REMARK 200 REJECTION CRITERIA (SIGMA(I)) : 0
REMARK 200
REMARK 200 OVERALL.
REMARK 200 COMPLETENESS FOR RANGE (%) : 95.5
REMARK 200 DATA REDUNDANCY : 4.0
REMARK 200 R MERGE (I) : NULL
REMARK 200 R SYM (I) : 0.041
REMARK 200 <I>/SIGMA(I)> FOR THE DATA SET : 20
REMARK 200
REMARK 200 IN THE HIGHEST RESOLUTION SHELL.
REMARK 200 HIGHEST RESOLUTION SHELL, RANGE HIGH (A) : 2.57
REMARK 200 HIGHEST RESOLUTION SHELL, RANGE LOW (A) : 2.73
REMARK 200 COMPLETENESS FOR SHELL (%) : 86.2
REMARK 200 DATA REDUNDANCY IN SHELL : 3.4
REMARK 200 R MERGE FOR SHELL (I) : NULL
REMARK 200 R SYM FOR SHELL (I) : 0.17
REMARK 200 <I>/SIGMA(I)> FOR SHELL : 4.3
REMARK 200
REMARK 200 DIFFRACTION PROTOCOL: MAD
REMARK 200 METHOD USED TO DETERMINE THE STRUCTURE: MAD
REMARK 200 SOFTWARE USED: NULL
REMARK 200 STARTING MODEL: NULL
REMARK 200
REMARK 200 REMARK: TWO WAVELENGTH HG MAD
REMARK 280
REMARK 280 CRYSTAL
REMARK 280 SOLVENT CONTENT, VS (%): 55
REMARK 280 MATTHEWS COEFFICIENT, VM (ANGSTROMS**3/DA): 3.1
REMARK 280
REMARK 280 CRYSTALLIZATION CONDITIONS:
REMARK 280 25% GLYCEROL, 15% PEG 4000, 50 MM TRIS PH 7.5,
REMARK 280 50 MM MGCL2, 20 MM CDCL2, 0.2 M KCL,
REMARK 280 1 MM DITHIOTHREITOL, 4 DEGREES C
REMARK 290
REMARK 290 CRYSTALLOGRAPHIC SYMMETRY
REMARK 290 SYMMETRY OPERATORS FOR SPACE GROUP: P 21 21 21
REMARK 290
REMARK 290 SYMOP SYMMETRY
REMARK 290 NNNMMM OPERATOR
REMARK 290 1555 X,Y,Z
REMARK 290 2555 1/2-X,-Y,1/2+Z

```

REMARK 290 3555 -X,1/2+Y,1/2-Z  
 REMARK 290 4555 1/2+X,1/2-Y,-Z  
 REMARK 290  
 REMARK 290 WHERE NNN -&GT; OPERATOR NUMBER  
 REMARK 290 MMM -&GT; TRANSLATION VECTOR  
 REMARK 290  
 REMARK 290 CRYSTALLOGRAPHIC SYMMETRY TRANSFORMATIONS

REMARK 290 THE FOLLOWING TRANSFORMATIONS OPERATE ON THE  
 ATOM/HETATM  
 RECORDS IN THIS ENTRY TO PRODUCE CRYSTALLOGRAPHICALLY

REMARK 290 RELATED MOLECULES.

REMARK 290	SMTRY1	1	1.000000	0.000000	0.000000	0.000000
REMARK 290	SMTRY2	1	0.000000	1.000000	0.000000	0.000000
REMARK 290	SMTRY3	1	0.000000	0.000000	1.000000	0.000000
REMARK 290	SMTRY1	2	-1.000000	0.000000	0.000000	31.94480
REMARK 290	SMTRY2	2	0.000000	-1.000000	0.000000	0.000000
REMARK 290	SMTRY3	2	0.000000	0.000000	1.000000	77.76050
REMARK 290	SMTRY1	3	-1.000000	0.000000	0.000000	0.000000
REMARK 290	SMTRY2	3	0.000000	1.000000	0.000000	42.13010
REMARK 290	SMTRY3	3	0.000000	0.000000	-1.000000	77.76050
REMARK 290	SMTRY1	4	1.000000	0.000000	0.000000	31.94480
REMARK 290	SMTRY2	4	0.000000	-1.000000	0.000000	42.13010
REMARK 290	SMTRY3	4	0.000000	0.000000	-1.000000	0.000000

REMARK 290

REMARK 290 REMARK: NULL

REMARK 295

REMARK 295 NON-CRYSTALLOGRAPHIC SYMMETRY

REMARK 295 THE TRANSFORMATIONS PRESENTED ON THE MTRIX RECORDS  
 BELOW

REMARK 295 DESCRIBE NON-CRYSTALLOGRAPHIC RELATIONSHIPS AMONG  
 ATOMS

REMARK 295 IN THIS ENTRY. APPLYING THE APPROPRIATE MTRIX

REMARK 295 TRANSFORMATION TO THE RESIDUES LISTED FIRST WILL YIELD

REMARK 295 APPROXIMATE COORDINATES FOR THE RESIDUES LISTED SECOND.

REMARK 295 CHAIN IDENTIFIERS GIVEN AS "?" REFER TO CHAINS FOR WHICH

REMARK 295 ATOMS ARE NOT FOUND IN THIS ENTRY.

REMARK 295

REMARK 295 APPLIED TO TRANSFORMED TO

REMARK 295 TRANSFORM CHAIN RESIDUES CHAIN RESIDUES RMSD

REMARK 295 SSS

REMARK 295

REMARK 465 IDENTIFIER; SSSEQ=SEQUENCE NUMBER; I=INSERTION CODE):

```
REMARK 465
REMARK 465 M RES C SSSEQI
REMARK 465 ALA A 2
REMARK 465 LYS A 3
REMARK 465 LYS A 4
REMARK 465 VAL A 5
REMARK 465 ALA A 6
REMARK 465 ALA A 7
REMARK 465 ASP A 141
REMARK 465 ALA B 2 TO ILE B 70
REMARK 465 ASP B 141
REMARK 470
REMARK 470 MISSING ATOM
REMARK 470 THE FOLLOWING RESIDUES HAVE MISSING ATOMS (M=MODEL
NUMBER;
REMARK 470 RES=RESIDUE NAME; C=CHAIN IDENTIFIER; SSEQ=SEQUENCE
NUMBER;
REMARK 470 I=INSERTION CODE):
REMARK 470 M RES CSSEQI ATOMS
REMARK 470 G C1051 P O1P O2P
REMARK 470 G D1051 P O1P O2P
REMARK 550
REMARK 550 SEGID
REMARK 550 RNA1, RNA2
REMARK 550 L111, L112
REMARK 600
REMARK 600 HETEROGEN
REMARK 600 THERE ARE A TOTAL OF 8 CADMIUM IONS IN THE STRUCTURE
REMARK 600
REMARK 600 THERE ARE A TOTAL OF 19 MAGNESIUM IONS IN THE STRUCTURE
```

REMARK 600  
REMARK 600 THERE ARE A TOTAL OF 8 METHYLMERCURY  
REMARK 600 IONS IN THE STRUCTURE.  
REMARK 600 THE METHYL GROUP HAS NOT BEEN MODELLED  
REMARK 600 FOR ANY OF THESE IONS.  
REMARK 600 TWO OF THE IONS ARE COVALENTLY BOUND  
REMARK 600 TO CYS A 39.  
REMARK 600 ONE IS COVALENTLY BOUND TO U C 1061.  
REMARK 600 ONE IS COVALENTLY BOUND TO U D 1061.  
REMARK 600  
REMARK 800  
REMARK 800 SITE  
REMARK 800 SITE\_IDENTIFIER: TSR  
REMARK 800 SITE\_DESCRIPTION:  
REMARK 800 PUTATIVE THIOSTREPTON/MICROCOCCIN BINDING SITE  
REMARK 800  
REMARK 800 SITE\_IDENTIFIER: TSR  
REMARK 800 SITE\_DESCRIPTION:  
REMARK 800 PUTATIVE THIOSTREPTON/MICROCOCCIN BINDING SITE  
REMARK 800  
REMARK 800 SITE\_IDENTIFIER: TSR  
REMARK 800 SITE\_DESCRIPTION:  
REMARK 800 PUTATIVE THIOSTREPTON/MICROCOCCIN BINDING SITE  
REMARK 800  
DBREF A 8 140 SWS P29395 RL11\_THEMA 1 141  
DBREF B 71 140 SWS P29395 RL11\_THEMA 1 141  
DBREF C 1051 1108 PDB 1051 1108  
DBREF D 1051 1108 PDB 1051 1108  
SEQADV RES C 1108 GI M67498 1168 ENGINEERED MUTATION  
SEQADV RES D 1108 GI M67498 1168 ENGINEERED MUTATION  
SEQRES 1 A 140 ALA LYS LYS VAL ALA ALA GLN ILE LYS LEU GLN LEU PRO  
SEQRES 2 A 140 ALA GLY LYS ALA THR PRO ALA PRO PRO VAL GLY PRO ALA  
  
SEQRES 3 A 140 LEU GLY GLN HIS GLY VAL ASN ILE MET GLU PHE CYS LYS  
SEQRES 4 A 140 ARG PHE ASN ALA GLU THR ALA ASP LYS ALA GLY MET ILE  
  
SEQRES 5 A 140 LEU PRO VAL VAL ILE THR VAL TYR GLU ASP LYS SER PHE  
SEQRES 6 A 140 THR PHE ILE ILE LYS THR PRO PRO ALA SER PHE LEU LEU  
SEQRES 7 A 140 LYS LYS ALA ALA GLY ILE GLU LYS GLY SER SER GLU PRO  
SEQRES 8 A 140 LYS ARG LYS ILE VAL GLY LYS VAL THR ARG LYS GLN ILE  
SEQRES 9 A 140 GLU GLU ILE ALA LYS THR LYS MET PRO ASP LEU ASN ALA  
SEQRES 10 A 140 ASN SER LEU GLU ALA ALA MET LYS ILE ILE GLU GLY THR  
SEQRES 11 A 140 ALA LYS SER MET GLY ILE GLU VAL VAL ASP  
SEQRES 1 B 140 ALA LYS LYS VAL ALA ALA GLN ILE LYS LEU GLN LEU PRO

HET	MG	375	0
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HET  MG  380  0
HET  MG  385  0
HET  MG  397  0
HET  MG  437  0  SEE REMARK 600
HET  HG  227  0
HET  HG  230  0
HET  HG  332  0
HET  HG  347  0
HET  HG  415  0
HET  HG  416  0
HET  HG  448  0
HET  HG  451  0  SEE REMARK 600
HETNAM  CD CD
HETNAM  MG MG
HETNAM  HG MMC
HETSYN  CD CADMIUM (II)
HETSYN  MG MAGNESIUM (II)
HETSYN  HG METHYLMERCURY ION
FORMUL  5  CD  8(CD1 2+)
FORMUL  6  MG  19(MG1 2+)
FORMUL  7  HG  8(C1 H3 HG1 1+)
FORMUL  8  HOH  *142(H2 O1)
HELIX  1  1 PRO A  26 GLN A  30  1  5
HELIX  2  2 ILE A  35 ALA A  47  1  13
HELIX  3  3 ALA A  75 ALA A  83  1  9
HELIX  4  4 ARG A 102 ASP A 115  1  14
HELIX  5  5 LEU A 121 SER A 134  1  14
HELIX  6  6 ALA B  75 ALA B  83  1  9
HELIX  7  7 ARG B 102 ASP B 115  1  14
HELIX  8  8 LEU B 121 MET B 135  1  15
SHEET  1  A 3 ILE A  9 PRO A 14  0
SHEET  2  A 3 ILE A 53 VAL A 60-1 N ILE A 58 O ILE A  9
SHEET  3  A 3 PHE A 66 ILE A 70-1 N ILE A 69 O VAL A 57
SHEET  1  B 2 GLY A 98 THR A 101  0
SHEET  2  B 2 ILE A 137 VAL A 140  1 N GLU A 138 O GLY A 98
SHEET  1  C 2 GLY B 98 VAL B 100  0
SHEET  2  C 2 ILE B 137 VAL B 139  1 N GLU B 138 O GLY B 98
SITE  1  TSR 2  A C1067  A C1095
SITE  2  TSR 2  A D1067  A D1095
SITE  3  TSR 3 PRO A 22 PRO A 23 PRO A 26
CRYST1  63.890  84.260 155.510 90.00 90.00 90.00 P 21 21 21  8
ORIGX1  1.000000  0.000000  0.000000  0.000000
ORIGX2  0.000000  1.000000  0.000000  0.000000
ORIGX3  0.000000  0.000000  1.000000  0.000000
SCALE1  0.015652  0.000000  0.000000  0.000000

```

SCALE2	0.000000	0.011868	0.000000	0.000000	
SCALE3	0.000000	0.000000	0.006430	0.000000	
MATRIX1	1	0.974505	0.101458	-0.200117	-4.54330 1
MATRIX2	1	0.097433	-0.994793	-0.029885	-3.74880 1
MATRIX3	1	-0.202107	0.009626	-0.979316	-50.69290 1
MATRIX1	2	0.973477	0.098780	-0.206364	-4.89630 1
MATRIX2	2	0.098758	-0.995057	-0.010432	-2.89050 1
MATRIX3	2	-0.206374	-0.010225	-0.978420	-50.97240 1
ATOM	1	N	GLN A 8	-7.803 -11.096 -9.783	1.00 71.77 L111 N
ATOM	2	CA	GLN A 8	-8.476 -9.887 -9.223	1.00 79.42 L111 C
ATOM	3	C	GLN A 8	-8.010 -8.599 -9.897	1.00 80.19 L111 C
ATOM	4	O	GLN A 8	-6.857 -8.190 -9.748	1.00 77.92 L111 O
ATOM	5	CB	GLN A 8	-8.212 -9.788 -7.722	1.00 79.86 L111 C
ATOM	6	CG	GLN A 8	-9.065 -8.752 -7.016	1.00 80.16 L111 C
ATOM	7	CD	GLN A 8	-9.072 -8.948 -5.518	1.00 80.58 L111 C
ATOM	8	OE1	GLN A 8	-8.020 -8.963 -4.881	1.00 82.16 L111 O
ATOM	9	NE2	GLN A 8	-10.261 -9.104 -4.946	1.00 79.20 L111 N
ATOM	10	N	ILE A 9	-8.916 -7.963 -10.634	1.00 81.13 L111 N
ATOM	11	CA	ILE A 9	-8.604 -6.723 -11.337	1.00 80.39 L111 C
ATOM	12	C	ILE A 9	-9.312 -5.530 -10.699	1.00 79.13 L111 C
ATOM	13	O	ILE A 9	-10.338 -5.680 -10.036	1.00 78.96 L111 O
ATOM	14	CB	ILE A 9	-9.013 -6.804 -12.834	1.00 77.02 L111 C
ATOM	15	CG1	ILE A 9	-10.534 -6.778 -12.970	1.00 77.57 L111 C
ATOM	16	CG2	ILE A 9	-8.482 -8.080 -13.452	1.00 74.06 L111 C
ATOM	17	CD1	ILE A 9	-11.066 -5.495 -13.552	1.00 83.48 L111 C
ATOM	18	N	LYS A 10	-8.752 -4.343 -10.900	1.00 80.87 L111 N
ATOM	19	CA	LYS A 10	-9.330 -3.121 -10.360	1.00 77.55 L111 C
ATOM	20	C	LYS A 10	-9.252 -2.011 -11.400	1.00 74.90 L111 C
ATOM	21	O	LYS A 10	-8.308 -1.945 -12.191	1.00 69.61 L111 O
ATOM	22	CB	LYS A 10	-8.590 -2.696 -9.089	1.00 78.72 L111 C
ATOM	23	CG	LYS A 10	-7.080 -2.607 -9.243	1.00 76.53 L111 C
ATOM	24	CD	LYS A 10	-6.482 -1.615 -8.256	1.00 76.55 L111 C
ATOM	25	CE	LYS A 10	-6.047 -2.300 -6.968	1.00 78.93 L111 C
ATOM	26	NZ	LYS A 10	-4.923 -1.584 -6.296	1.00 81.54 L111 N
ATOM	27	N	LEU A 11	-10.261 -1.149 -11.403	1.00 72.26 L111 N
ATOM	28	CA	LEU A 11	-10.311 -0.037 -12.342	1.00 77.13 L111 C
ATOM	29	C	LEU A 11	-11.286 1.024 -11.852	1.00 78.99 L111 C
ATOM	30	O	LEU A 11	-12.052 0.790 -10.915	1.00 78.52 L111 O
ATOM	31	CB	LEU A 11	-10.744 -0.525 -13.728	1.00 77.54 L111 C
ATOM	32	CG	LEU A 11	-11.051 -2.014 -13.906	1.00 72.58 L111 C
ATOM	33	CD1	LEU A 11	-12.511 -2.199 -14.290	1.00 68.73 L111 C
ATOM	34	CD2	LEU A 11	-10.128 -2.590 -14.969	1.00 73.75 L111 C
ATOM	35	N	GLN A 12	-11.255 2.189 -12.489	1.00 80.79 L111 N
ATOM	36	CA	GLN A 12	-12.144 3.284 -12.120	1.00 82.10 L111 C
ATOM	37	C	GLN A 12	-13.115 3.582 -13.261	1.00 80.51 L111 C



ATOM	83	CA	THR	A	19	-18.843	-1.936	-22.089	1.00	98.62	L111	C
ATOM	84	C	THR	A	19	-17.834	-1.538	-23.177	1.00	98.30	L111	C
ATOM	85	O	THR	A	19	-17.439	-2.379	-23.987	1.00	94.28	L111	O
ATOM	86	CB	THR	A	19	-20.250	-2.000	-22.756	1.00	100.00	L111	C
ATOM	87	OG1	THR	A	19	-21.255	-2.212	-21.753	1.00	100.00	L111	O
ATOM	88	CG2	THR	A	19	-20.311	-3.135	-23.772	1.00	99.76	L111	C
ATOM	89	N	PRO	A	20	-17.392	-0.267	-23.212	1.00	100.00	L111	N
ATOM	90	CA	PRO	A	20	-16.433	0.087	-24.268	1.00	100.00	L111	C
ATOM	91	C	PRO	A	20	-15.174	-0.778	-24.289	1.00	100.00	L111	C
ATOM	92	O	PRO	A	20	-14.692	-1.220	-23.246	1.00	100.00	L111	O
ATOM	93	CB	PRO	A	20	-16.117	1.561	-23.995	1.00	100.00	L111	C
ATOM	94	CG	PRO	A	20	-16.510	1.782	-22.568	1.00	100.00	L111	C
ATOM	95	CD	PRO	A	20	-17.690	0.887	-22.347	1.00	100.00	L111	C
ATOM	96	N	ALA	A	21	-14.650	-1.015	-25.487	1.00	100.00	L111	N
ATOM	97	CA	ALA	A	21	-13.450	-1.823	-25.640	1.00	100.00	L111	C
ATOM	98	C	ALA	A	21	-12.238	-1.115	-25.030	1.00	100.00	L111	C
ATOM	99	O	ALA	A	21	-11.622	-1.626	-24.097	1.00	100.00	L111	O
ATOM	100	CB	ALA	A	21	-13.204	-2.130	-27.121	1.00	100.00	L111	C
ATOM	101	N	PRO	A	22	-11.886	0.079	-25.542	1.00	100.00	L111	N
ATOM	102	CA	PRO	A	22	-10.725	0.773	-24.969	1.00	100.00	L111	C
ATOM	103	C	PRO	A	22	-10.740	0.904	-23.434	1.00	100.00	L111	C
ATOM	104	O	PRO	A	22	-9.793	0.478	-22.768	1.00	100.00	L111	O
ATOM	105	CB	PRO	A	22	-10.726	2.127	-25.683	1.00	100.00	L111	C
ATOM	106	CG	PRO	A	22	-11.439	1.862	-26.979	1.00	100.00	L111	C
ATOM	107	CD	PRO	A	22	-12.496	0.845	-26.645	1.00	100.00	L111	C
ATOM	108	N	PRO	A	23	-11.807	1.495	-22.853	1.00	100.00	L111	N
ATOM	109	CA	PRO	A	23	-11.880	1.650	-21.390	1.00	100.00	L111	C
ATOM	110	C	PRO	A	23	-11.941	0.338	-20.592	1.00	100.00	L111	C
ATOM	111	O	PRO	A	23	-11.025	0.026	-19.829	1.00	100.00	L111	O
ATOM	112	CB	PRO	A	23	-13.135	2.507	-21.173	1.00	99.53	L111	C
ATOM	113	CG	PRO	A	23	-13.446	3.100	-22.519	1.00	100.00	L111	C
ATOM	114	CD	PRO	A	23	-12.988	2.077	-23.513	1.00	100.00	L111	C
ATOM	115	N	VAL	A	24	-13.020	-0.423	-20.767	1.00	100.00	L111	N
ATOM	116	CA	VAL	A	24	-13.199	-1.689	-20.051	1.00	95.98	L111	C
ATOM	117	C	VAL	A	24	-12.711	-2.903	-20.844	1.00	94.54	L111	C
ATOM	118	O	VAL	A	24	-11.538	-3.272	-20.773	1.00	88.41	L111	O
ATOM	119	CB	VAL	A	24	-14.688	-1.923	-19.689	1.00	92.89	L111	C
ATOM	120	CG1	VAL	A	24	-14.809	-2.320	-18.232	1.00	90.90	L111	C
ATOM	121	CG2	VAL	A	24	-15.504	-0.668	-19.969				



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ATOM 173 N VAL A 33 -13.107 -12.509 -17.415 1.00 89.92 L111 N
ATOM 174 CA VAL A 33 -14.376 -11.822 -17.196 1.00 90.50 L111 C
ATOM 175 C VAL A 33 -15.254 -11.711 -18.443 1.00 88.55 L111 C
ATOM 176 O VAL A 33 -14.753 -11.581 -19.560 1.00 88.34 L111 O
ATOM 177 CB VAL A 33 -14.135 -10.398 -16.652 1.00 92.08 L111 C
ATOM 178 CG1 VAL A 33 -15.292 -9.976 -15.770 1.00 90.59 L111 C
ATOM 179 CG2 VAL A 33 -12.830 -10.351 -15.873 1.00 93.31 L111 C
ATOM 180 N ASN A 34 -16.568 -11.766 -18.237 1.00 89.80 L111 N
ATOM 181 CA ASN A 34 -17.533 -11.650 -19.327 1.00 94.89 L111 C
ATOM 182 C ASN A 34 -18.128 -10.245 -19.290 1.00 96.48 L111 C
ATOM 183 O ASN A 34 -19.141 -10.008 -18.630 1.00 97.04 L111 O
ATOM 184 CB ASN A 34 -18.661 -12.681 -19.182 1.00 97.83 L111 C
ATOM 185 CG ASN A 34 -18.405 -13.683 -18.072 1.00 100.00 L111 C
ATOM 186 OD1 ASN A 34 -19.205 -13.813 -17.141 1.00 100.00 L111 O
ATOM 187 ND2 ASN A 34 -17.291 -14.405 -18.167 1.00 100.00 L111 N
ATOM 188 N ILE A 35 -17.486 -9.325 -20.006 1.00 98.20 L111 N
ATOM 189 CA ILE A 35 -17.898 -7.922 -20.071 1.00 97.32 L111 C
ATOM 190 C ILE A 35 -19.392 -7.651 -19.844 1.00 99.75 L111 C
ATOM 191 O ILE A 35 -19.776 -7.148 -18.788 1.00 100.00 L111 O
ATOM 192 CB ILE A 35 -17.478 -7.282 -21.426 1.00 95.15 L111 C
ATOM 193 CG1 ILE A 35 -16.341 -8.094 -22.064 1.00 93.73 L111 C
ATOM 194 CG2 ILE A 35 -17.066 -5.823 -21.213 1.00 87.68 L111 C
ATOM 195 CD1 ILE A 35 -14.960 -7.824 -21.485 1.00 91.66 L111 C
ATOM 196 N MET A 36 -20.220 -7.980 -20.835 1.00 100.00 L111 N
ATOM 197 CA MET A 36 -21.672 -7.767 -20.773 1.00 99.82 L111 C
ATOM 198 C MET A 36 -22.294 -7.868 -19.376 1.00 97.54 L111 C
ATOM 199 O MET A 36 -23.032 -6.975 -18.950 1.00 95.12 L111 O
ATOM 200 CB MET A 36 -22.384 -8.752 -21.713 1.00 100.00 L111 C
ATOM 201 CG MET A 36 -23.911 -8.645 -21.709 1.00 100.00 L111 C
ATOM 202 SD MET A 36 -24.759 -10.248 -21.810 1.00 100.00 L111 S
ATOM 203 CE MET A 36 -25.601 -10.300 -20.213 1.00 97.00 L111 C
ATOM 204 N GLU A 37 -22.001 -8.960 -18.674 1.00 95.35 L111 N
ATOM 205 CA GLU A 37 -22.535 -9.190 -17.335 1.00 92.68 L111 C
ATOM 206 C GLU A 37 -22.124 -8.100 -16.349 1.00 93.66 L111 C
ATOM 207 O GLU A 37 -22.925 -7.672 -15.515 1.00 91.34 L111 O
ATOM 208 CB GLU A 37 -22.071 -10.552 -16.819 1.00 90.67 L111 C
ATOM 209 CG GLU A 37 -23.205 -11.512 -16.511 1.00 93.38 L111 C
ATOM 210 CD GLU A 37 -22.929 -12.372 -15.290 1.00 96.55 L111 C
ATOM 211 OE1 GLU A 37 -22.044 -13.254 -15.365 1.00 91.81 L111 O
ATOM 212 OE2 GLU A 37 -23.600 -12.163 -14.256 1.00 99.15 L111 O
ATOM 213 N PHE A 38 -20.872 -7.657 -16.449 1.00 94.99 L111 N
ATOM 214 CA PHE A 38 -20.335 -6.614 -15.575 1.00 95.14 L111 C
ATOM 215 C PHE A 38 -20.928 -5.243 -15.907 1.00 93.32 L111 C
ATOM 216 O PHE A 38 -21.382 -4.527 -15.017 1.00 92.65 L111 O
ATOM 217 CB PHE A 38 -18.802 -6.565 -15.693 1.00 93.51 L111 C

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ATOM	218	CG PHE A 38	-18.139	-5.586	-14.748	1.00	96.97	L111 C
ATOM	219	CD1 PHE A 38	-18.716	-5.269	-13.518	1.00	98.99	L111 C
ATOM	220	CD2 PHE A 38	-16.935	-4.978	-15.094	1.00	96.40	L111 C
ATOM	221	CE1 PHE A 38	-18.106	-4.355	-12.651	1.00	95.25	L111 C
ATOM	222	CE2 PHE A 38	-16.318	-4.064	-14.233	1.00	96.95	L111 C
ATOM	223	CZ PHE A 38	-16.905	-3.754	-13.010	1.00	92.93	L111 C
ATOM	224	N CYS A 39	-20.925	-4.884	-17.187	1.00	94.43	L111 N
ATOM	225	CA CYS A 39	-21.461	-3.597	-17.632	1.00	95.64	L111 C
ATOM	226	C CYS A 39	-22.840	-3.321	-17.044	1.00	96.32	L111 C
ATOM	227	O CYS A 39	-23.051	-2.295	-16.392	1.00	95.48	L111 O
ATOM	228	CB CYS A 39	-21.540	-3.563	-19.159	1.00	93.89	L111 C
ATOM	229	SG CYS A 39	-19.986	-3.992	-19.971	1.00	100.00	L111 S
ATOM	230	N LYS A 40	-23.774	-4.239	-17.279	1.00	96.81	L111 N
ATOM	231	CA LYS A 40	-25.133	-4.101	-16.768	1.00	96.22	L111 C
ATOM	232	C LYS A 40	-25.135	-4.168	-15.240	1.00	95.74	L111 C
ATOM	233	O LYS A 40	-25.823	-3.389	-14.576	1.00	96.26	L111 O
ATOM	234	CB LYS A 40	-26.029	-5.205	-17.339	1.00	95.66	L111 C
ATOM	235	CG LYS A 40	-25.956	-5.344	-18.855	1.00	97.68	L111 C
ATOM	236	CD LYS A 40	-27.132	-6.148	-19.401	1.00	95.99	L111 C
ATOM	237	CE LYS A 40	-26.947	-6.475	-20.880	1.00	94.18	L111 C
ATOM	238	NZ LYS A 40	-28.171	-6.189	-21.684	1.00	88.70	L111 N
ATOM	239	N ARG A 41	-24.356	-5.097	-14.688	1.00	92.53	L111 N
ATOM	240	CA ARG A 41	-24.262	-5.260	-13.239	1.00	89.97	L111 C
ATOM	241	C ARG A 41	-23.694	-4.003	-12.582	1.00	90.13	L111 C
ATOM	242	O ARG A 41	-24.306	-3.433	-11.679	1.00	91.63	L111 O
ATOM	243	CB ARG A 41	-23.375	-6.459	-12.900	1.00	85.72	L111 C
ATOM	244	CG ARG A 41	-24.143	-7.710	-12.526	1.00	85.51	L111 C
ATOM	245	CD ARG A 41	-23.330	-8.594	-11.595	1.00	90.22	L111 C
ATOM	246	NE ARG A 41	-22.610	-9.641	-12.318	1.00	88.90	L111 N
ATOM	247	CZ ARG A 41	-21.670	-10.412	-11.778	1.00	87.28	L111 C
ATOM	248	NH1 ARG A 41	-21.332	-10.257	-10.501	1.00	84.21	L111 N
ATOM	249	NH2 ARG A 41	-21.070	-11.340	-12.511	1.00	80.87	L111 N
ATOM	250	N PHE A 42	-22.517	-3.583	-13.037	1.00	87.95	L111 N
ATOM	251	CA PHE A 42	-21.865	-2.393	-12.509	1.00	82.17	L111 C
ATOM	252	C PHE A 42	-22.838	-1.228	-12.587	1.00	83.84	L111 C
ATOM	253	O PHE A 42	-23.215	-0.648	-11.566	1.00	84.64	L111 O
ATOM	254	CB PHE A 42	-20.608	-2.074	-13.325	1.00	78.71	L111 C
ATOM	255	CG PHE A 42	-19.934	-0.792	-12.925	1.00	83.84	L111 C
ATOM	256	CD1 PHE A 42	-19.109	-0.745	-11.802	1.00	84.59	L111 C
ATOM	257	CD2 PHE A 42	-20.132	0.373	-13.662	1.00	83.65	L111 C
ATOM	258	CE1 PHE A 42	-18.490	0.444	-11.417	1.00	79.21	L111 C
ATOM	259	CE2 PHE A 42	-19.518	1.567	-13.289	1.00	77.97	L111 C
ATOM	260	CZ PHE A 42	-18.695	1.602	-12.162	1.00	81.55	L111 C
ATOM	261	N ASN A 43	-23.253	-0.906	-13.808	1.00	85.30	L111 N
ATOM	262	CA ASN A 43	-24.181	0.191	-14.053	1.00	86.52	L111 C

ATOM	263	C	ASN A 43	-25.488	0.062	-13.284	1.00	85.43	L111 C
ATOM	264	O	ASN A 43	-26.281	1.000	-13.240	1.00	85.51	L111 O
ATOM	265	CB	ASN A 43	-24.476	0.296	-15.548	1.00	86.27	L111 C
ATOM	266	CG	ASN A 43	-23.265	0.716	-16.344	1.00	92.38	L111 C
ATOM	267	OD1	ASN A 43	-22.347	1.340	-15.811	1.00	96.74	L111 O
ATOM	268	ND2	ASN A 43	-23.249	0.374	-17.627	1.00	99.06	L111 N
ATOM	269	N	ALA A 44	-25.712	-1.098	-12.679	1.00	85.49	L111 N
ATOM	270	CA	ALA A 44	-26.930	-1.319	-11.912	1.00	84.79	L111 C
ATOM	271	C	ALA A 44	-26.900	-0.515	-10.618	1.00	85.21	L111 C
ATOM	272	O	ALA A 44	-27.668	0.433	-10.452	1.00	84.84	L111 O
ATOM	273	CB	ALA A 44	-27.092	-2.797	-11.603	1.00	86.85	L111 C
ATOM	274	N	GLU A 45	-26.005	-0.893	-9.708	1.00	85.98	L111 N
ATOM	275	CA	GLU A 45	-25.885	-0.211	-8.420	1.00	90.10	L111 C
ATOM	276	C	GLU A 45	-25.222	1.158	-8.536	1.00	89.46	L111 C
ATOM	277	O	GLU A 45	-25.388	2.010	-7.661	1.00	88.02	L111 O
ATOM	278	CB	GLU A 45	-25.103	-1.076	-7.427	1.00	89.91	L111 C
ATOM	279	CG	GLU A 45	-23.812	-1.641	-7.983	1.00	93.26	L111 C
ATOM	280	CD	GLU A 45	-23.917	-3.118	-8.293	1.00	95.55	L111 C
ATOM	281	OE1	GLU A 45	-24.558	-3.844	-7.503	1.00	94.41	L111 O
ATOM	282	OE2	GLU A 45	-23.360	-3.551	-9.326	1.00	98.04	L111 O
ATOM	283	N	THR A 46	-24.463	1.369	-9.608	1.00	89.00	L111 N
ATOM	284	CA	THR A 46	-23.806	2.655	-9.810	1.00	91.97	L111 C
ATOM	285	C	THR A 46	-24.849	3.680	-10.261	1.00	95.20	L111 C
ATOM	286	O	THR A 46	-24.516	4.737	-10.806	1.00	95.92	L111 O
ATOM	287	CB	THR A 46	-22.681	2.560	-10.865	1.00	90.40	L111 C
ATOM	288	OG1	THR A 46	-23.232	2.170	-12.129	1.00	88.41	L111 O
ATOM	289	CG2	THR A 46	-21.634	1.545	-10.429	1.00	87.67	L111 C
ATOM	290	N	ALA A 47	-26.116	3.343	-10.031	1.00	95.70	L111 N
ATOM	291	CA	ALA A 47	-27.237	4.208	-10.374	1.00	93.30	L111 C
ATOM	292	C	ALA A 47	-27.464	5.142	-9.191	1.00	95.59	L111 C
ATOM	293	O	ALA A 47	-27.681	6.341	-9.367	1.00	97.14	L111 O
ATOM	294	CB	ALA A 47	-28.488	3.373	-10.634	1.00	85.02	L111 C
ATOM	295	N	ASP A 48	-27.409	4.580	-7.985	1.00	98.95	L111 N
ATOM	296	CA	ASP A 48	-27.589	5.360	-6.764	1.00	100.00	L111 C
ATOM	297	C	ASP A 48	-26.667	6.582	-6.823	1.00	100.00	L111 C
ATOM	298	O	ASP A 48	-27.065	7.697	-6.477	1.00	100.00	L111 O
ATOM	299	CB	ASP A 48	-27.248	4.515	-5.526	1.00	100.00	L111 C
ATOM	300	CG	ASP A 48	-27.577	3.038	-5.706	1.00	100.00	L111 C
ATOM	301	OD1	ASP A 48	-28.633	2.721	-6.297	1.00	100.00	L111 O
ATOM	302	OD2	ASP A 48	-26.777	2.191	-5.249	1.00	100.00	L111 O
ATOM	303	N	LYS A 49	-25.434	6.356	-7.270	1.00	100.00	L111 N
ATOM	304	CA	LYS A 49	-24.440	7.419	-7.394	1.00	99.10	L111 C
ATOM	305	C	LYS A 49	-24.009	7.547	-8.859	1.00	98.06	L111 C
ATOM	306	O	LYS A 49	-23.106	6.842	-9.318	1.00	95.26	L111 O
ATOM	307	CB	LYS A 49	-23.226	7.105	-6.512	1.00	94.97	L111 C

TOTAL: 5086660



ATOM	308	CG	LYS	A	49	-23.561	6.908	-5.037	1.00	92.57	L111	C
ATOM	309	CD	LYS	A	49	-22.956	5.619	-4.498	1.00	93.51	L111	C
ATOM	310	CE	LYS	A	49	-21.611	5.873	-3.827	1.00	94.40	L111	C
ATOM	311	NZ	LYS	A	49	-20.528	4.998	-4.365	1.00	88.97	L111	N
ATOM	312	N	ALA	A	50	-24.661	8.450	-9.587	1.00	95.33	L111	N
ATOM	313	CA	ALA	A	50	-24.360	8.653	-10.999	1.00	93.02	L111	C
ATOM	314	C	ALA	A	50	-23.680	9.985	-11.305	1.00	91.25	L111	C
ATOM	315	O	ALA	A	50	-23.898	10.986	-10.619	1.00	90.14	L111	O
ATOM	316	CB	ALA	A	50	-25.636	8.522	-11.819	1.00	96.51	L111	C
ATOM	317	N	GLY	A	51	-22.861	9.984	-12.353	1.00	89.39	L111	N
ATOM	318	CA	GLY	A	51	-22.153	11.186	-12.752	1.00	90.09	L111	C
ATOM	319	C	GLY	A	51	-20.709	11.173	-12.289	1.00	91.40	L111	C
ATOM	320	O	GLY	A	51	-19.828	11.733	-12.943	1.00	91.06	L111	O
ATOM	321	N	MET	A	52	-20.465	10.520	-11.158	1.00	91.81	L111	N
ATOM	322	CA	MET	A	52	-19.125	10.440	-10.591	1.00	88.05	L111	C
ATOM	323	C	MET	A	52	-18.347	9.218	-11.062	1.00	84.95	L111	C
ATOM	324	O	MET	A	52	-18.927	8.206	-11.455	1.00	85.89	L111	O
ATOM	325	CB	MET	A	52	-19.207	10.425	-9.065	1.00	85.66	L111	C
ATOM	326	CG	MET	A	52	-20.358	11.236	-8.503	1.00	86.98	L111	C
ATOM	327	SD	MET	A	52	-20.028	11.840	-6.840	1.00	94.43	L111	S
ATOM	328	CE	MET	A	52	-18.414	12.577	-7.060	1.00	92.32	L111	C
ATOM	329	N	ILE	A	53	-17.025	9.330	-11.021	1.00	80.70	L111	N
ATOM	330	CA	ILE	A	53	-16.145	8.242	-11.415	1.00	76.40	L111	C
ATOM	331	C	ILE	A	53	-15.856	7.437	-10.157	1.00	76.01	L111	C
ATOM	332	O	ILE	A	53	-15.214	7.937	-9.238	1.00	80.34	L111	O
ATOM	333	CB	ILE	A	53	-14.815	8.781	-11.987	1.00	72.67	L111	C
ATOM	334	CG1	ILE	A	53	-15.035	9.279	-13.421	1.00	73.66	L111	C
ATOM	335	CG2	ILE	A	53	-13.735	7.706	-11.897	1.00	69.87	L111	C
ATOM	336	CD1	ILE	A	53	-14.073	8.712	-14.461	1.00	67.81	L111	C
ATOM	337	N	LEU	A	54	-16.337	6.199	-10.110	1.00	77.62	L111	N
ATOM	338	CA	LEU	A	54	-16.123	5.355	-8.940	1.00	75.31	L111	C
ATOM	339	C	LEU	A	54	-15.263	4.129	-9.242	1.00	73.26	L111	C
ATOM	340	O	LEU	A	54	-15.468	3.448	-10.248	1.00	69.71	L111	O
ATOM	341	CB	LEU	A	54	-17.471	4.913	-8.354	1.00	74.18	L111	C
ATOM	342	CG	LEU	A	54	-18.446	4.186	-9.283	1.00	76.71	L111	C
ATOM	343	CD1	LEU	A	54	-19.398	3.339	-8.456	1.00	78.50	L111	C
ATOM	344	CD2	LEU	A	54	-19.221	5.196	-10.112	1.00	77.50	L111	C
ATOM	345	N	PRO	A	55	-14.277	3.841	-8.368	1.00	73.50	L111	N
ATOM	346	CA	PRO	A	55	-13.379	2.694	-8.531	1.00	73.63	L111	C
ATOM	347	C	PRO	A	55	-13.998	1.397	-8.010	1.00	72.99	L111	C
ATOM	348	O	PRO	A	55	-14.516	1.349	-6.895	1.00	76.87	L111	O
ATOM	349	CB	PRO	A	55	-12.139	3.096	-7.736	1.00	69.02	L111	C
ATOM	350	CG	PRO	A	55	-12.654	4.000	-6.669	1.00	66.68	L111	C
ATOM	351	CD	PRO	A	55	-13.950	4.617	-7.157	1.00	72.43	L111	C
ATOM	352	N	VAL	A	56	-13.945	0.349	-8.825	1.00	70.25	L111	N

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ATOM	398	CZ	TYR	A	61	-15.489	-14.526	-6.214	1.00	92.07	L111	C
ATOM	399	OH	TYR	A	61	-15.910	-13.543	-5.347	1.00	94.51	L111	O
ATOM	400	N	GLU	A	62	-11.666	-18.936	-10.557	1.00	89.59	L111	N
ATOM	401	CA	GLU	A	62	-11.218	-19.921	-11.541	1.00	86.30	L111	C
ATOM	402	C	GLU	A	62	-12.248	-20.245	-12.626	1.00	84.38	L111	C
ATOM	403	O	GLU	A	62	-11.886	-20.480	-13.779	1.00	83.12	L111	O
ATOM	404	CB	GLU	A	62	-10.798	-21.217	-10.835	1.00	86.59	L111	C
ATOM	405	CG	GLU	A	62	-11.842	-21.781	-9.872	1.00	98.78	L111	C
ATOM	406	CD	GLU	A	62	-12.709	-22.865	-10.502	1.00	100.00	L111	C
ATOM	407	OE1	GLU	A	62	-12.149	-23.866	-11.007	1.00	100.00	L111	O
ATOM	408	OE2	GLU	A	62	-13.952	-22.711	-10.490	1.00	100.00	L111	O
ATOM	409	N	ASP	A	63	-13.527	-20.246	-12.261	1.00	83.04	L111	N
ATOM	410	CA	ASP	A	63	-14.593	-20.554	-13.210	1.00	83.65	L111	C
ATOM	411	C	ASP	A	63	-15.045	-19.360	-14.066	1.00	89.63	L111	C
ATOM	412	O	ASP	A	63	-16.153	-19.364	-14.609	1.00	90.46	L111	O
ATOM	413	CB	ASP	A	63	-15.795	-21.132	-12.461	1.00	80.07	L111	C
ATOM	414	CG	ASP	A	63	-16.738	-20.061	-11.968	1.00	79.27	L111	C
ATOM	415	OD1	ASP	A	63	-16.275	-19.146	-11.254	1.00	85.70	L111	O
ATOM	416	OD2	ASP	A	63	-17.941	-20.130	-12.298	1.00	76.37	L111	O
ATOM	417	N	LYS	A	64	-14.188	-18.347	-14.185	1.00	91.01	L111	N
ATOM	418	CA	LYS	A	64	-14.481	-17.150	-14.976	1.00	89.76	L111	C
ATOM	419	C	LYS	A	64	-15.585	-16.261	-14.398	1.00	89.42	L111	C
ATOM	420	O	LYS	A	64	-15.809	-15.149	-14.882	1.00	91.74	L111	O
ATOM	421	CB	LYS	A	64	-14.833	-17.540	-16.418	1.00	92.48	L111	C
ATOM	422	CG	LYS	A	64	-13.737	-17.237	-17.436	1.00	92.64	L111	C
ATOM	423	CD	LYS	A	64	-12.362	-17.682	-16.936	1.00	89.88	L111	C
ATOM	424	CE	LYS	A	64	-11.520	-18.269	-18.060	1.00	87.02	L111	C
ATOM	425	NZ	LYS	A	64	-12.331	-18.548	-19.280	1.00	89.34	L111	N
ATOM	426	N	SER	A	65	-16.280	-16.748	-13.373	1.00	88.30	L111	N
ATOM	427	CA	SER	A	65	-17.336	-15.966	-12.738	1.00	87.60	L111	C
ATOM	428	C	SER	A	65	-16.668	-14.827	-11.979	1.00	90.25	L111	C
ATOM	429	O	SER	A	65	-15.443	-14.800	-11.857	1.00	94.42	L111	O
ATOM	430	CB	SER	A	65	-18.138	-16.830	-11.766	1.00	83.90	L111	C
ATOM	431	OG	SER	A	65	-19.255	-16.115	-11.265	1.00	86.12	L111	O
ATOM	432	N	PHE	A	66	-17.459	-13.895	-11.456	1.00	89.68	L111	N
ATOM	433	CA	PHE	A	66	-16.872	-12.769	-10.737	1.00	86.65	L111	C
ATOM	434	C	PHE	A	66	-17.824	-11.963	-9.852	1.00	84.85	L111	C
ATOM	435	O	PHE	A	66	-19.049	-12.065	-9.956	1.00	84.96	L111	O
ATOM	436	CB	PHE	A	66	-16.207	-11.819	-11.740	1.00	83.79	L111	C
ATOM	437	CG	PHE	A	66	-17.166	-11.224	-12.736	1.00	84.15	L111	C
ATOM	438	CD1	PHE	A	66	-17.849	-10.044	-12.446	1.00	84.23	L111	C
ATOM	439	CD2	PHE	A	66	-17.402	-11.851	-13.955	1.00	85.47	L111	C
ATOM	440	CE1	PHE	A	66	-18.756	-9.496	-13.358	1.00	83.49	L111	C
ATOM	441	CE2	PHE	A	66	-18.307	-11.312	-14.875	1.00	85.83	L111	C
ATOM	442	CZ	PHE	A	66	-18.985	-10.132	-14.574	1.00	81.40	L111	C

ATOM	443	N	THR A 67	-17.223	-11.166	-8.975	1.00	83.77	L111 N
ATOM	444	CA	THR A 67	-17.937	-10.279	-8.065	1.00	79.66	L111 C
ATOM	445	C	THR A 67	-17.102	-9.009	-8.062	1.00	79.21	L111 C
ATOM	446	O	THR A 67	-16.005	-8.985	-8.623	1.00	78.86	L111 O
ATOM	447	CB	THR A 67	-17.990	-10.835	-6.630	1.00	77.12	L111 C
ATOM	448	OG1	THR A 67	-16.660	-11.101	-6.169	1.00	71.17	L111 O
ATOM	449	CG2	THR A 67	-18.807	-12.112	-6.585	1.00	76.03	L111 C
ATOM	450	N	PHE A 68	-17.603	-7.954	-7.439	1.00	77.92	L111 N
ATOM	451	CA	PHE A 68	-16.850	-6.711	-7.409	1.00	76.33	L111 C
ATOM	452	C	PHE A 68	-17.396	-5.750	-6.379	1.00	74.52	L111 C
ATOM	453	O	PHE A 68	-18.609	-5.594	-6.241	1.00	74.74	L111 O
ATOM	454	CB	PHE A 68	-16.871	-6.046	-8.789	1.00	79.76	L111 C
ATOM	455	CG	PHE A 68	-18.255	-5.772	-9.311	1.00	78.43	L111 C
ATOM	456	CD1	PHE A 68	-18.994	-6.781	-9.922	1.00	77.56	L111 C
ATOM	457	CD2	PHE A 68	-18.821	-4.506	-9.193	1.00	77.06	L111 C
ATOM	458	CE1	PHE A 68	-20.276	-6.532	-10.409	1.00	79.65	L111 C
ATOM	459	CE2	PHE A 68	-20.103	-4.247	-9.677	1.00	76.90	L111 C
ATOM	460	CZ	PHE A 68	-20.831	-5.263	-10.285	1.00	77.56	L111 C
ATOM	461	N	ILE A 69	-16.491	-5.105	-5.656	1.00	73.94	L111 N
ATOM	462	CA	ILE A 69	-16.885	-4.142	-4.644	1.00	70.90	L111 C
ATOM	463	C	ILE A 69	-16.752	-2.736	-5.218	1.00	71.09	L111 C
ATOM	464	O	ILE A 69	-15.773	-2.420	-5.901	1.00	68.28	L111 O
ATOM	465	CB	ILE A 69	-16.010	-4.273	-3.377	1.00	65.36	L111 C
ATOM	466	CG1	ILE A 69	-14.550	-3.966	-3.709	1.00	63.63	L111 C
ATOM	467	CG2	ILE A 69	-16.119	-5.682	-2.820	1.00	61.98	L111 C
ATOM	468	CD1	ILE A 69	-13.850	-3.146	-2.650	1.00	54.75	L111 C
ATOM	469	N	ILE A 70	-17.753	-1.903	-4.962	1.00	68.20	L111 N
ATOM	470	CA	ILE A 70	-17.740	-0.530	-5.443	1.00	65.88	L111 C
ATOM	471	C	ILE A 70	-17.350	0.388	-4.283	1.00	61.84	L111 C
ATOM	472	O	ILE A 70	-17.975	0.367	-3.222	1.00	60.58	L111 O
ATOM	473	CB	ILE A 70	-19.126	-0.135	-6.022	1.00	66.46	L111 C
ATOM	474	CG1	ILE A 70	-19.030	-0.026	-7.545	1.00	67.64	L111 C
ATOM	475	CG2	ILE A 70	-19.608	1.187	-5.432	1.00	69.87	L111 C
ATOM	476	CD1	ILE A 70	-19.695	-1.163	-8.283	1.00	63.00	L111 C
ATOM	477	N	LYS A 71	-16.301	1.179	-4.489	1.00	55.49	L111 N
ATOM	478	CA	LYS A 71	-15.820	2.092	-3.463	1.00	49.56	L111 C
ATOM	479	C	LYS A 71	-16.181	3.531	-3.773	1.00	51.89	L111 C
ATOM	480	O	LYS A 71	-16.814	3.826	-4.787	1.00	58.09	L111 O
ATOM	481	CB	LYS A 71	-14.301	1.996	-3.325	1.00	41.23	L111 C
ATOM	482	CG	LYS A 71	-13.736	0.617	-3.549	1.00	45.62	L111 C
ATOM	483	CD	LYS A 71	-12.280	0.573	-3.134	1.00	47.82	L111 C
ATOM	484	CE	LYS A 71	-12.066	-0.371	-1.962	1.00	53.59	L111 C
ATOM	485	NZ	LYS A 71	-10.785	-1.130	-2.085	1.00	54.56	L111 N
ATOM	486	N	THR A 72	-15.763	4.424	-2.883	1.00	51.64	L111 N
ATOM	487	CA	THR A 72	-16.005	5.851	-3.034	1.00	48.54	L111 C

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ATOM	488	C	THR	A	72	-15.040	6.390	-4.088	1.00	47.19	L111	C
ATOM	489	O	THR	A	72	-13.919	5.896	-4.227	1.00	51.43	L111	O
ATOM	490	CB	THR	A	72	-15.758	6.584	-1.711	1.00	49.44	L111	C
ATOM	491	OG1	THR	A	72	-14.374	6.469	-1.356	1.00	56.76	L111	O
ATOM	492	CG2	THR	A	72	-16.598	5.975	-0.602	1.00	49.50	L111	C
ATOM	493	N	PRO	A	73	-15.463	7.409	-4.850	1.00	43.35	L111	N
ATOM	494	CA	PRO	A	73	-14.603	7.989	-5.890	1.00	39.98	L111	C
ATOM	495	C	PRO	A	73	-13.260	8.487	-5.357	1.00	38.40	L111	C
ATOM	496	O	PRO	A	73	-13.153	8.908	-4.206	1.00	41.41	L111	O
ATOM	497	CB	PRO	A	73	-15.449	9.117	-6.483	1.00	40.56	L111	C
ATOM	498	CG	PRO	A	73	-16.536	9.360	-5.490	1.00	44.56	L111	C
ATOM	499	CD	PRO	A	73	-16.775	8.071	-4.781	1.00	42.40	L111	C
ATOM	500	N	PRO	A	74	-12.217	8.453	-6.198	1.00	36.48	L111	N
ATOM	501	CA	PRO	A	74	-10.882	8.904	-5.788	1.00	35.21	L111	C
ATOM	502	C	PRO	A	74	-10.881	10.296	-5.162	1.00	32.68	L111	C
ATOM	503	O	PRO	A	74	-11.778	11.102	-5.406	1.00	30.40	L111	O
ATOM	504	CB	PRO	A	74	-10.066	8.856	-7.082	1.00	37.87	L111	C
ATOM	505	CG	PRO	A	74	-10.787	7.880	-7.956	1.00	31.11	L111	C
ATOM	506	CD	PRO	A	74	-12.244	8.000	-7.601	1.00	35.28	L111	C
ATOM	507	N	ALA	A	75	-9.868	10.570	-4.348	1.00	31.58	L111	N
ATOM	508	CA	ALA	A	75	-9.763	11.862	-3.698	1.00	29.59	L111	C
ATOM	509	C	ALA	A	75	-9.517	12.901	-4.774	1.00	34.00	L111	C
ATOM	510	O	ALA	A	75	-10.210	13.915	-4.837	1.00	37.52	L111	O
ATOM	511	CB	ALA	A	75	-8.618	11.856	-2.694	1.00	34.28	L111	C
ATOM	512	N	SER	A	76	-8.532	12.638	-5.627	1.00	30.09	L111	N
ATOM	513	CA	SER	A	76	-8.211	13.561	-6.702	1.00	31.31	L111	C
ATOM	514	C	SER	A	76	-9.467	13.929	-7.483	1.00	31.25	L111	C
ATOM	515	O	SER	A	76	-9.661	15.091	-7.825	1.00	36.66	L111	O
ATOM	516	CB	SER	A	76	-7.169	12.951	-7.643	1.00	32.45	L111	C
ATOM	517	OG	SER	A	76	-7.473	11.608	-7.957	1.00	36.38	L111	O
ATOM	518	N	PHE	A	77	-10.323	12.946	-7.752	1.00	31.85	L111	N
ATOM	519	CA	PHE	A	77	-11.564	13.194	-8.489	1.00	34.16	L111	C
ATOM	520	C	PHE	A	77	-12.502	14.125	-7.734	1.00	38.37	L111	C
ATOM	521	O	PHE	A	77	-12.919	15.160	-8.251	1.00	41.67	L111	O
ATOM	522	CB	PHE	A	77	-12.307	11.894	-8.769	1.00	33.17	L111	C
ATOM	523	CG	PHE	A	77	-13.623	12.095	-9.468	1.00	40.76	L111	C
ATOM	524	CD1	PHE	A	77	-13.667	12.357	-10.837	1.00	47.11	L111	C
ATOM	525	CD2	PHE	A	77	-14.818	12.034	-8.761	1.00	42.42	L111	C
ATOM	526	CE1	PHE	A	77	-14.880	12.554	-11.492	1.00	38.82	L111	C
ATOM	527	CE2	PHE	A	77	-16.041	12.230	-9.409	1.00	42.68	L111	C
ATOM	528	CZ	PHE	A	77	-16.069	12.491	-10.777	1.00	38.85	L111	C
ATOM	529	N	LEU	A	78	-12.852	13.743	-6.514	1.00	39.27	L111	N
ATOM	530	CA	LEU	A	78	-13.732	14.568	-5.703	1.00	42.01	L111	C
ATOM	531	C	LEU	A	78	-13.162	15.986	-5.625	1.00	44.64	L111	C
ATOM	532	O	LEU	A	78	-13.892	16.967	-5.777	1.00	45.86	L111	O

ATOM	533	CB	LEU	A	78	-13.861	13.966	-4.303	1.00	42.80	L111	C
ATOM	534	CG	LEU	A	78	-14.640	12.646	-4.258	1.00	47.12	L111	C
ATOM	535	CD1	LEU	A	78	-14.485	11.973	-2.899	1.00	38.14	L111	C
ATOM	536	CD2	LEU	A	78	-16.108	12.925	-4.548	1.00	50.88	L111	C
ATOM	537	N	LEU	A	79	-11.851	16.081	-5.406	1.00	43.07	L111	N
ATOM	538	CA	LEU	A	79	-11.164	17.367	-5.309	1.00	34.91	L111	C
ATOM	539	C	LEU	A	79	-11.352	18.182	-6.580	1.00	35.68	L111	C
ATOM	540	O	LEU	A	79	-11.701	19.355	-6.522	1.00	36.29	L111	O
ATOM	541	CB	LEU	A	79	-9.676	17.150	-5.056	1.00	32.85	L111	C
ATOM	542	CG	LEU	A	79	-9.326	16.833	-3.603	1.00	29.72	L111	C
ATOM	543	CD1	LEU	A	79	-7.848	16.529	-3.480	1.00	33.33	L111	C
ATOM	544	CD2	LEU	A	79	-9.703	18.013	-2.730	1.00	29.46	L111	C
ATOM	545	N	LYS	A	80	-11.113	17.558	-7.727	1.00	39.06	L111	N
ATOM	546	CA	LYS	A	80	-11.292	18.235	-9.006	1.00	38.30	L111	C
ATOM	547	C	LYS	A	80	-12.692	18.832	-8.990	1.00	39.56	L111	C
ATOM	548	O	LYS	A	80	-12.872	20.036	-9.144	1.00	44.34	L111	O
ATOM	549	CB	LYS	A	80	-11.191	17.239	-10.163	1.00	32.02	L111	C
ATOM	550	CG	LYS	A	80	-9.805	17.066	-10.750	1.00	32.26	L111	C
ATOM	551	CD	LYS	A	80	-9.758	15.821	-11.628	1.00	37.75	L111	C
ATOM	552	CE	LYS	A	80	-8.410	15.660	-12.313	1.00	49.50	L111	C
ATOM	553	NZ	LYS	A	80	-8.046	14.224	-12.490	1.00	54.98	L111	N
ATOM	554	N	LYS	A	81	-13.681	17.969	-8.789	1.00	39.53	L111	N
ATOM	555	CA	LYS	A	81	-15.070	18.386	-8.754	1.00	38.23	L111	C
ATOM	556	C	LYS	A	81	-15.268	19.576	-7.832	1.00	41.10	L111	C
ATOM	557	O	LYS	A	81	-15.797	20.603	-8.242	1.00	50.63	L111	O
ATOM	558	CB	LYS	A	81	-15.949	17.230	-8.290	1.00	40.15	L111	C
ATOM	559	CG	LYS	A	81	-17.433	17.521	-8.367	1.00	56.64	L111	C
ATOM	560	CD	LYS	A	81	-18.209	16.317	-8.878	1.00	68.16	L111	C
ATOM	561	CE	LYS	A	81	-19.133	15.761	-7.799	1.00	76.64	L111	C
ATOM	562	NZ	LYS	A	81	-18.420	15.535	-6.502	1.00	78.09	L111	N
ATOM	563	N	ALA	A	82	-14.836	19.435	-6.585	1.00	45.28	L111	N
ATOM	564	CA	ALA	A	82	-14.976	20.500	-5.598	1.00	43.40	L111	C
ATOM	565	C	ALA	A	82	-14.384	21.832	-6.056	1.00	49.00	L111	C
ATOM	566	O	ALA	A	82	-15.003	22.884	-5.892	1.00	53.59	L111	O
ATOM	567	CB	ALA	A	82	-14.330	20.076	-4.290	1.00	42.16	L111	C
ATOM	568	N	ALA	A	83	-13.183	21.790	-6.621	1.00	48.31	L111	N
ATOM	569	CA	ALA	A	83	-12.527	23.004	-7.089	1.00	44.61	L111	C
ATOM	570	C	ALA	A	83	-13.115	23.458	-8.416	1.00	44.02	L111	C
ATOM	571	O	ALA	A	83	-12.693						

ATOM	578	CA	ILE A 85	-11.715	22.219	-12.334	1.00	37.65	L111 C
ATOM	579	C	ILE A 85	-11.826	20.868	-13.037	1.00	41.62	L111 C
ATOM	580	O	ILE A 85	-12.532	19.974	-12.571	1.00	45.50	L111 O
ATOM	581	CB	ILE A 85	-10.261	22.429	-11.863	1.00	37.93	L111 C
ATOM	582	CG1	ILE A 85	-9.905	21.408	-10.784	1.00	32.73	L111 C
ATOM	583	CG2	ILE A 85	-10.088	23.845	-11.336	1.00	42.04	L111 C
ATOM	584	CD1	ILE A 85	-8.435	21.395	-10.442	1.00	22.67	L111 C
ATOM	585	N	GLU A 86	-11.126	20.728	-14.159	1.00	45.67	L111 N
ATOM	586	CA	GLU A 86	-11.156	19.499	-14.948	1.00	47.13	L111 C
ATOM	587	C	GLU A 86	-9.874	18.675	-14.831	1.00	47.71	L111 C
ATOM	588	O	GLU A 86	-9.882	17.460	-15.044	1.00	48.51	L111 O
ATOM	589	CB	GLU A 86	-11.408	19.839	-16.421	1.00	57.79	L111 C
ATOM	590	CG	GLU A 86	-12.374	18.896	-17.128	1.00	77.13	L111 C
ATOM	591	CD	GLU A 86	-13.815	19.383	-17.078	1.00	86.58	L111 C
ATOM	592	OE1	GLU A 86	-14.025	20.594	-16.849	1.00	90.24	L111 O
ATOM	593	OE2	GLU A 86	-14.734	18.553	-17.268	1.00	89.81	L111 O
ATOM	594	N	LYS A 87	-8.771	19.335	-14.499	1.00	39.94	L111 N
ATOM	595	CA	LYS A 87	-7.499	18.645	-14.366	1.00	38.76	L111 C
ATOM	596	C	LYS A 87	-6.699	19.204	-13.204	1.00	34.61	L111 C
ATOM	597	O	LYS A 87	-6.981	20.291	-12.715	1.00	46.69	L111 O
ATOM	598	CB	LYS A 87	-6.686	18.784	-15.656	1.00	41.37	L111 C
ATOM	599	CG	LYS A 87	-7.279	18.057	-16.847	1.00	47.04	L111 C
ATOM	600	CD	LYS A 87	-6.550	18.426	-18.128	1.00	53.23	L111 C
ATOM	601	CE	LYS A 87	-5.833	17.224	-18.724	1.00	60.76	L111 C
ATOM	602	NZ	LYS A 87	-6.109	15.961	-17.979	1.00	61.63	L111 N
ATOM	603	N	GLY A 88	-5.703	18.452	-12.759	1.00	34.29	L111 N
ATOM	604	CA	GLY A 88	-4.871	18.914	-11.669	1.00	33.53	L111 C
ATOM	605	C	GLY A 88	-3.718	19.688	-12.261	1.00	35.94	L111 C
ATOM	606	O	GLY A 88	-3.422	19.547	-13.445	1.00	37.03	L111 O
ATOM	607	N	SER A 89	-3.065	20.511	-11.453	1.00	35.86	L111 N
ATOM	608	CA	SER A 89	-1.941	21.285	-11.951	1.00	31.79	L111 C
ATOM	609	C	SER A 89	-0.968	20.358	-12.658	1.00	33.45	L111 C
ATOM	610	O	SER A 89	-0.868	19.185	-12.317	1.00	36.12	L111 O
ATOM	611	CB	SER A 89	-1.227	21.987	-10.801	1.00	30.17	L111 C
ATOM	612	OG	SER A 89	0.141	22.195	-11.114	1.00	29.65	L111 O
ATOM	613	N	SER A 90	-0.260	20.881	-13.651	1.00	36.82	L111 N
ATOM	614	CA	SER A 90	0.716	20.083	-14.372	1.00	35.62	L111 C
ATOM	615	C	SER A 90	1.981	20.112	-13.530	1.00	35.74	L111 C
ATOM	616	O	SER A 90	2.879	19.287	-13.692	1.00	37.58	L111 O
ATOM	617	CB	SER A 90	0.976	20.682	-15.758	1.00	37.33	L111 C
ATOM	618	OG	SER A 90	1.955	21.708	-15.701	1.00	51.94	L111 O
ATOM	619	N	GLU A 91	2.034	21.083	-12.625	1.00	33.32	L111 N
ATOM	620	CA	GLU A 91	3.166	21.246	-11.726	1.00	38.55	L111 C
ATOM	621	C	GLU A 91	2.619	21.648	-10.362	1.00	37.86	L111 C
ATOM	622	O	GLU A 91	2.553	22.832	-10.026	1.00	36.53	L111 O

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ATOM	713	NE	ARG A 102	-10.495	23.786	9.006	1.00	86.85	L111 N
ATOM	714	CZ	ARG A 102	-10.080	23.304	10.174	1.00	96.04	L111 C
ATOM	715	NH1	ARG A 102	-9.710	22.033	10.275	1.00	95.91	L111 N
ATOM	716	NH2	ARG A 102	-10.033	24.095	11.242	1.00	96.71	L111 N
ATOM	717	N	LYS A 103	-14.103	23.514	4.626	1.00	50.48	L111 N
ATOM	718	CA	LYS A 103	-15.341	22.774	4.811	1.00	51.76	L111 C
ATOM	719	C	LYS A 103	-15.441	21.718	3.719	1.00	51.34	L111 C
ATOM	720	O	LYS A 103	-15.884	20.600	3.966	1.00	59.36	L111 O
ATOM	721	CB	LYS A 103	-16.545	23.721	4.751	1.00	53.67	L111 C
ATOM	722	CG	LYS A 103	-17.839	23.135	5.319	1.00	62.90	L111 C
ATOM	723	CD	LYS A 103	-17.717	22.781	6.806	1.00	65.48	L111 C
ATOM	724	CE	LYS A 103	-18.840	21.841	7.257	1.00	63.76	L111 C
ATOM	725	NZ	LYS A 103	-19.077	21.884	8.732	1.00	58.26	L111 N
ATOM	726	N	GLN A 104	-15.013	22.073	2.512	1.00	51.89	L111 N
ATOM	727	CA	GLN A 104	-15.052	21.145	1.388	1.00	44.08	L111 C
ATOM	728	C	GLN A 104	-14.161	19.939	1.664	1.00	42.43	L111 C
ATOM	729	O	GLN A 104	-14.519	18.804	1.347	1.00	40.53	L111 O
ATOM	730	CB	GLN A 104	-14.602	21.850	0.110	1.00	42.64	L111 C
ATOM	731	CG	GLN A 104	-15.663	22.751	-0.484	1.00	35.82	L111 C
ATOM	732	CD	GLN A 104	-15.242	23.354	-1.804	1.00	44.67	L111 C
ATOM	733	OE1	GLN A 104	-14.303	24.154	-1.867	1.00	37.53	L111 O
ATOM	734	NE2	GLN A 104	-15.936	22.975	-2.873	1.00	35.39	L111 N
ATOM	735	N	ILE A 105	-12.998	20.186	2.254	1.00	39.32	L111 N
ATOM	736	CA	ILE A 105	-12.088	19.103	2.584	1.00	35.57	L111 C
ATOM	737	C	ILE A 105	-12.846	18.187	3.525	1.00	41.32	L111 C
ATOM	738	O	ILE A 105	-12.770	16.965	3.411	1.00	46.00	L111 O
ATOM	739	CB	ILE A 105	-10.832	19.624	3.298	1.00	33.68	L111 C
ATOM	740	CG1	ILE A 105	-9.873	20.242	2.277	1.00	32.96	L111 C
ATOM	741	CG2	ILE A 105	-10.154	18.495	4.061	1.00	34.33	L111 C
ATOM	742	CD1	ILE A 105	-9.501	19.321	1.131	1.00	34.42	L111 C
ATOM	743	N	GLU A 106	-13.584	18.800	4.448	1.00	47.08	L111 N
ATOM	744	CA	GLU A 106	-14.382	18.068	5.428	1.00	53.52	L111 C
ATOM	745	C	GLU A 106	-15.411	17.186	4.719	1.00	55.13	L111 C
ATOM	746	O	GLU A 106	-15.606	16.027	5.087	1.00	59.36	L111 O
ATOM	747	CB	GLU A 106	-15.094	19.051	6.381	1.00	50.72	L111 C
ATOM	748	CG	GLU A 106	-15.480	18.464	7.748	1.00	55.56	L111 C
ATOM	749	CD	GLU A 106	-16.029	19.504	8.734	1.00	62.03	L111 C
ATOM	750	OE1	GLU A 106	-15.308	20.476	9.054	1.00	63.26	L111 O
ATOM	751	OE2	GLU A 106	-17.182	19.345	9.199	1.00	53.90	L111 O
ATOM	752	N	GLU A 107	-16.061	17.731	3.695	1.00	51.75	L111 N
ATOM	753	CA	GLU A 107	-17.071	16.982	2.954	1.00	52.07	L111 C
ATOM	754	C	GLU A 107	-16.476	15.755	2.282	1.00	50.13	L111 C
ATOM	755	O	GLU A 107	-16.990	14.642	2.417	1.00	49.53	L111 O
ATOM	756	CB	GLU A 107	-17.720	17.871	1.891	1.00	56.84	L111 C
ATOM	757	CG	GLU A 107	-17.859	19.328	2.293	1.00	73.20	L111 C

ATOM	758	CD	GLU	A	107	-18.843	20.088	1.422	1.00	81.27	L111 C
ATOM	759	OE1	GLU	A	107	-19.271	19.540	0.382	1.00	84.05	L111 O
ATOM	760	OE2	GLU	A	107	-19.187	21.237	1.779	1.00	86.15	L111 O
ATOM	761	N	ILE	A	108	-15.391	15.973	1.549	1.00	46.89	L111 N
ATOM	762	CA	ILE	A	108	-14.719	14.900	0.844	1.00	39.41	L111 C
ATOM	763	C	ILE	A	108	-14.222	13.854	1.829	1.00	40.77	L111 C
ATOM	764	O	ILE	A	108	-14.441	12.658	1.637	1.00	43.65	L111 O
ATOM	765	CB	ILE	A	108	-13.542	15.447	0.019	1.00	38.05	L111 C
ATOM	766	CG1	ILE	A	108	-14.072	16.428	-1.032	1.00	36.44	L111 C
ATOM	767	CG2	ILE	A	108	-12.796	14.305	-0.649	1.00	41.19	L111 C
ATOM	768	CD1	ILE	A	108	-13.004	17.084	-1.882	1.00	31.78	L111 C
ATOM	769	N	ALA	A	109	-13.561	14.303	2.891	1.00	40.57	L111 N
ATOM	770	CA	ALA	A	109	-13.053	13.380	3.895	1.00	42.41	L111 C
ATOM	771	C	ALA	A	109	-14.205	12.546	4.429	1.00	44.77	L111 C
ATOM	772	O	ALA	A	109	-14.051	11.356	4.685	1.00	48.40	L111 O
ATOM	773	CB	ALA	A	109	-12.393	14.140	5.032	1.00	38.72	L111 C
ATOM	774	N	LYS	A	110	-15.365	13.174	4.589	1.00	47.97	L111 N
ATOM	775	CA	LYS	A	110	-16.537	12.474	5.099	1.00	44.59	L111 C
ATOM	776	C	LYS	A	110	-17.027	11.474	4.066	1.00	45.30	L111 C
ATOM	777	O	LYS	A	110	-17.377	10.342	4.401	1.00	44.67	L111 O
ATOM	778	CB	LYS	A	110	-17.651	13.469	5.422	1.00	45.45	L111 C
ATOM	779	CG	LYS	A	110	-17.991	13.562	6.902	1.00	47.29	L111 C
ATOM	780	CD	LYS	A	110	-17.733	14.963	7.448	1.00	51.84	L111 C
ATOM	781	CE	LYS	A	110	-18.991	15.558	8.070	1.00	53.58	L111 C
ATOM	782	NZ	LYS	A	110	-18.712	16.257	9.356	1.00	55.16	L111 N
ATOM	783	N	THR	A	111	-17.043	11.902	2.807	1.00	44.49	L111 N
ATOM	784	CA	THR	A	111	-17.492	11.060	1.705	1.00	42.63	L111 C
ATOM	785	C	THR	A	111	-16.635	9.810	1.548	1.00	44.42	L111 C
ATOM	786	O	THR	A	111	-17.149	8.707	1.375	1.00	44.77	L111 O
ATOM	787	CB	THR	A	111	-17.452	11.830	0.376	1.00	40.13	L111 C
ATOM	788	OG1	THR	A	111	-18.545	12.754	0.325	1.00	46.15	L111 O
ATOM	789	CG2	THR	A	111	-17.552	10.871	-0.799	1.00	43.65	L111 C
ATOM	790	N	LYS	A	112	-15.323	9.995	1.609	1.00	42.25	L111 N
ATOM	791	CA	LYS	A	112	-14.382	8.898	1.448	1.00	42.77	L111 C
ATOM	792	C	LYS	A	112	-14.081	8.127	2.732	1.00	43.93	L111 C
ATOM	793	O	LYS	A	112	-13.321	7.157	2.713	1.00	47.28	L111 O
ATOM	794	CB	LYS	A	112	-13.072	9.442	0.873	1.00	44.33	L111 C
ATOM	795	CG	LYS	A	112	-13.129	9.772	-0.607	1.00	40.93	L111 C
ATOM	796	CD	LYS	A	112	-11.806	9.474	-1.281	1.00	35.66	L111 C
ATOM	797	CE	LYS	A	112	-11.377	8.032	-1.062			

ATOM	803	CB	MET A 113	-15.410	8.457	6.177	1.00	39.84	L111 C
ATOM	804	CG	MET A 113	-14.931	8.283	7.609	1.00	45.81	L111 C
ATOM	805	SD	MET A 113	-13.481	9.269	8.040	1.00	47.31	L111 S
ATOM	806	CE	MET A 113	-14.261	10.787	8.610	1.00	49.60	L111 C
ATOM	807	N	PRO A 114	-15.524	5.793	4.484	1.00	32.93	L111 N
ATOM	808	CA	PRO A 114	-15.582	4.328	4.458	1.00	29.51	L111 C
ATOM	809	C	PRO A 114	-14.301	3.703	3.912	1.00	35.05	L111 C
ATOM	810	O	PRO A 114	-13.918	2.609	4.314	1.00	41.74	L111 O
ATOM	811	CB	PRO A 114	-16.791	4.013	3.575	1.00	27.80	L111 C
ATOM	812	CG	PRO A 114	-17.214	5.307	2.967	1.00	23.57	L111 C
ATOM	813	CD	PRO A 114	-16.678	6.411	3.811	1.00	31.92	L111 C
ATOM	814	N	ASP A 115	-13.629	4.408	3.008	1.00	38.82	L111 N
ATOM	815	CA	ASP A 115	-12.399	3.898	2.419	1.00	36.41	L111 C
ATOM	816	C	ASP A 115	-11.138	4.462	3.069	1.00	36.55	L111 C
ATOM	817	O	ASP A 115	-10.025	4.080	2.713	1.00	40.35	L111 O
ATOM	818	CB	ASP A 115	-12.385	4.193	0.919	1.00	48.68	L111 C
ATOM	819	CG	ASP A 115	-13.453	3.418	0.162	1.00	57.41	L111 C
ATOM	820	OD1	ASP A 115	-13.653	2.221	0.464	1.00	51.55	L111 O
ATOM	821	OD2	ASP A 115	-14.090	4.009	-0.737	1.00	58.21	L111 O
ATOM	822	N	LEU A 116	-11.311	5.368	4.024	1.00	38.89	L111 N
ATOM	823	CA	LEU A 116	-10.178	5.969	4.720	1.00	33.57	L111 C
ATOM	824	C	LEU A 116	-9.916	5.199	6.007	1.00	32.97	L111 C
ATOM	825	O	LEU A 116	-10.817	4.567	6.547	1.00	40.69	L111 O
ATOM	826	CB	LEU A 116	-10.482	7.427	5.055	1.00	38.53	L111 C
ATOM	827	CG	LEU A 116	-9.930	8.533	4.156	1.00	37.13	L111 C
ATOM	828	CD1	LEU A 116	-9.839	8.062	2.720	1.00	34.98	L111 C
ATOM	829	CD2	LEU A 116	-10.837	9.742	4.261	1.00	33.33	L111 C
ATOM	830	N	ASN A 117	-8.686	5.256	6.501	1.00	32.67	L111 N
ATOM	831	CA	ASN A 117	-8.336	4.549	7.725	1.00	33.28	L111 C
ATOM	832	C	ASN A 117	-8.052	5.502	8.889	1.00	39.76	L111 C
ATOM	833	O	ASN A 117	-7.373	5.140	9.851	1.00	36.63	L111 O
ATOM	834	CB	ASN A 117	-7.117	3.666	7.475	1.00	23.35	L111 C
ATOM	835	CG	ASN A 117	-5.872	4.470	7.208	1.00	24.02	L111 C
ATOM	836	OD1	ASN A 117	-5.949	5.659	6.916	1.00	31.18	L111 O
ATOM	837	ND2	ASN A 117	-4.714	3.828	7.306	1.00	18.87	L111 N
ATOM	838	N	ALA A 118	-8.572	6.720	8.799	1.00	41.20	L111 N
ATOM	839	CA	ALA A 118	-8.363	7.710	9.846	1.00	41.18	L111 C
ATOM	840	C	ALA A 118	-9.297	7.443	11.018	1.00	43.82	L111 C
ATOM	841	O	ALA A 118	-10.455	7.069	10.827	1.00	45.81	L111 O
ATOM	842	CB	ALA A 118	-8.604	9.103	9.296	1.00	41.30	L111 C
ATOM	843	N	ASN A 119	-8.793	7.644	12.230	1.00	42.07	L111 N
ATOM	844	CA	ASN A 119	-9.589	7.419	13.429	1.00	42.41	L111 C
ATOM	845	C	ASN A 119	-10.370	8.660	13.847	1.00	48.14	L111 C
ATOM	846	O	ASN A 119	-11.141	8.625	14.807	1.00	53.14	L111 O
ATOM	847	CB	ASN A 119	-8.684	6.981	14.575	1.00	37.27	L111 C

ATOM	848	CG ASN A 119	-8.180	5.575	14.400	1.00	33.45	L111 C
ATOM	849	OD1 ASN A 119	-8.886	4.714	13.876	1.00	31.47	L111 O
ATOM	850	ND2 ASN A 119	-6.951	5.328	14.837	1.00	38.73	L111 N
ATOM	851	N SER A 120	-10.168	9.756	13.125	1.00	48.44	L111 N
ATOM	852	CA SER A 120	-10.851	11.005	13.430	1.00	43.86	L111 C
ATOM	853	C SER A 120	-11.091	11.809	12.163	1.00	45.90	L111 C
ATOM	854	O SER A 120	-10.321	11.715	11.208	1.00	53.71	L111 O
ATOM	855	CB SER A 120	-10.010	11.834	14.401	1.00	38.80	L111 C
ATOM	856	OG SER A 120	-8.642	11.834	14.030	1.00	32.06	L111 O
ATOM	857	N LEU A 121	-12.157	12.601	12.156	1.00	46.97	L111 N
ATOM	858	CA LEU A 121	-12.476	13.429	11.000	1.00	44.83	L111 C
ATOM	859	C LEU A 121	-11.297	14.333	10.678	1.00	45.31	L111 C
ATOM	860	O LEU A 121	-11.078	14.693	9.526	1.00	52.25	L111 O
ATOM	861	CB LEU A 121	-13.705	14.291	11.277	1.00	39.77	L111 C
ATOM	862	CG LEU A 121	-13.904	15.469	10.325	1.00	41.18	L111 C
ATOM	863	CD1 LEU A 121	-14.063	14.958	8.900	1.00	41.06	L111 C
ATOM	864	CD2 LEU A 121	-15.128	16.260	10.751	1.00	41.00	L111 C
ATOM	865	N GLU A 122	-10.542	14.701	11.705	1.00	46.54	L111 N
ATOM	866	CA GLU A 122	-9.383	15.562	11.522	1.00	47.46	L111 C
ATOM	867	C GLU A 122	-8.327	14.834	10.702	1.00	45.12	L111 C
ATOM	868	O GLU A 122	-7.781	15.383	9.747	1.00	51.65	L111 O
ATOM	869	CB GLU A 122	-8.807	15.962	12.881	1.00	45.32	L111 C
ATOM	870	CG GLU A 122	-9.646	16.987	13.629	1.00	57.78	L111 C
ATOM	871	CD GLU A 122	-10.643	16.353	14.588	1.00	63.03	L111 C
ATOM	872	OE1 GLU A 122	-10.380	15.234	15.075	1.00	64.43	L111 O
ATOM	873	OE2 GLU A 122	-11.690	16.979	14.857	1.00	69.35	L111 O
ATOM	874	N ALA A 123	-8.045	13.593	11.083	1.00	41.17	L111 N
ATOM	875	CA ALA A 123	-7.062	12.786	10.381	1.00	38.97	L111 C
ATOM	876	C ALA A 123	-7.516	12.566	8.944	1.00	41.17	L111 C
ATOM	877	O ALA A 123	-6.701	12.562	8.022	1.00	41.16	L111 O
ATOM	878	CB ALA A 123	-6.891	11.452	11.081	1.00	36.50	L111 C
ATOM	879	N ALA A 124	-8.822	12.389	8.760	1.00	36.64	L111 N
ATOM	880	CA ALA A 124	-9.390	12.168	7.432	1.00	36.26	L111 C
ATOM	881	C ALA A 124	-9.133	13.362	6.533	1.00	35.14	L111 C
ATOM	882	O ALA A 124	-8.742	13.207	5.379	1.00	41.09	L111 O
ATOM	883	CB ALA A 124	-10.886	11.914	7.533	1.00	32.82	L111 C
ATOM	884	N MET A 125	-9.358	14.555	7.072	1.00	38.73	L111 N
ATOM	885	CA MET A 125	-9.158	15.785	6.322	1.00	34.84	L111 C
ATOM	886	C MET A 125	-7.686	15.968	6.003	1.00	31.87	L111 C
ATOM	887	O MET A 125	-7.330	16.458	4.938	1.00	42.09	L111 O
ATOM	888	CB MET A 125	-9.671	16.977	7.126	1.00	35.51	L111 C
ATOM	889	CG MET A 125	-11.072	16.769	7.695	1.00	40.88	L111 C
ATOM	890	SD MET A 125	-12.008	18.287	7.948	1.00	45.99	L111 S
ATOM	891	CE MET A 125	-10.675	19.462	8.286	1.00	44.96	L111 C
ATOM	892	N LYS A 126	-6.831	15.567	6.930	1.00	28.09	L111 N



ATOM	938	CA	ALA A 132	-5.096	18.292	-2.835	1.00	26.64	L111 C
ATOM	939	C	ALA A 132	-3.753	18.974	-3.058	1.00	28.30	L111 C
ATOM	940	O	ALA A 132	-3.524	19.602	-4.084	1.00	30.29	L111 O
ATOM	941	CB	ALA A 132	-5.954	19.134	-1.922	1.00	32.54	L111 C
ATOM	942	N	LYS A 133	-2.866	18.843	-2.082	1.00	29.52	L111 N
ATOM	943	CA	LYS A 133	-1.545	19.443	-2.158	1.00	27.21	L111 C
ATOM	944	C	LYS A 133	-0.754	18.848	-3.311	1.00	30.72	L111 C
ATOM	945	O	LYS A 133	0.190	19.458	-3.813	1.00	34.77	L111 O
ATOM	946	CB	LYS A 133	-0.784	19.205	-0.846	1.00	30.61	L111 C
ATOM	947	CG	LYS A 133	-0.843	20.371	0.138	1.00	38.23	L111 C
ATOM	948	CD	LYS A 133	-0.782	19.897	1.581	1.00	35.27	L111 C
ATOM	949	CE	LYS A 133	0.653	19.826	2.079	1.00	45.39	L111 C
ATOM	950	NZ	LYS A 133	0.737	19.680	3.568	1.00	50.50	L111 N
ATOM	951	N	SER A 134	-1.141	17.650	-3.729	1.00	31.51	L111 N
ATOM	952	CA	SER A 134	-0.441	16.966	-4.807	1.00	33.04	L111 C
ATOM	953	C	SER A 134	-0.969	17.300	-6.202	1.00	30.13	L111 C
ATOM	954	O	SER A 134	-0.345	16.952	-7.198	1.00	27.50	L111 O
ATOM	955	CB	SER A 134	-0.510	15.452	-4.588	1.00	31.88	L111 C
ATOM	956	OG	SER A 134	-1.741	14.927	-5.055	1.00	23.70	L111 O
ATOM	957	N	MET A 135	-2.107	17.977	-6.276	1.00	26.88	L111 N
ATOM	958	CA	MET A 135	-2.691	18.308	-7.563	1.00	25.82	L111 C
ATOM	959	C	MET A 135	-2.887	19.801	-7.783	1.00	31.45	L111 C
ATOM	960	O	MET A 135	-3.737	20.209	-8.581	1.00	30.19	L111 O
ATOM	961	CB	MET A 135	-4.029	17.597	-7.711	1.00	27.23	L111 C
ATOM	962	CG	MET A 135	-4.974	17.857	-6.574	1.00	22.80	L111 C
ATOM	963	SD	MET A 135	-6.230	16.597	-6.491	1.00	37.09	L111 S
ATOM	964	CE	MET A 135	-7.008	16.793	-8.089	1.00	41.07	L111 C
ATOM	965	N	GLY A 136	-2.105	20.613	-7.078	1.00	27.82	L111 N
ATOM	966	CA	GLY A 136	-2.215	22.050	-7.228	1.00	22.84	L111 C
ATOM	967	C	GLY A 136	-3.569	22.630	-6.854	1.00	27.99	L111 C
ATOM	968	O	GLY A 136	-4.068	23.538	-7.515	1.00	33.90	L111 O
ATOM	969	N	ILE A 137	-4.181	22.099	-5.806	1.00	27.75	L111 N
ATOM	970	CA	ILE A 137	-5.458	22.621	-5.345	1.00	29.45	L111 C
ATOM	971	C	ILE A 137	-5.207	23.141	-3.934	1.00	37.77	L111 C
ATOM	972	O	ILE A 137	-4.722	22.409	-3.066	1.00	42.44	L111 O
ATOM	973	CB	ILE A 137	-6.553	21.535	-5.334	1.00	29.74	L111 C
ATOM	974	CG1	ILE A 137	-6.755	20.994	-6.751	1.00	30.99	L111 C
ATOM	975	CG2	ILE A 137	-7.864	22.117	-4.842	1.00	21.17	L111 C
ATOM	976	CD1	ILE A 137	-7.883	19.989	-6.877	1.00	23.63	L111 C
ATOM	977	N	GLU A 138	-5.508	24.419	-3.723	1.00	40.79	L111 N
ATOM	978	CA	GLU A 138	-5.299	25.058	-2.435	1.00	39.24	L111 C
ATOM	979	C	GLU A 138	-6.528	25.003	-1.549	1.00	43.73	L111 C
ATOM	980	O	GLU A 138	-7.640	24.799	-2.031	1.00	48.97	L111 O
ATOM	981	CB	GLU A 138	-4.903	26.506				

ATOM	983	CD	GLU A 138	-3.094	28.228	-2.556	1.00	67.14	L111 C
ATOM	984	OE1	GLU A 138	-3.950	28.970	-3.098	1.00	59.01	L111 O
ATOM	985	OE2	GLU A 138	-1.950	28.613	-2.220	1.00	67.00	L111 O
ATOM	986	N	VAL A 139	-6.316	25.193	-0.251	1.00	48.03	L111 N
ATOM	987	CA	VAL A 139	-7.404	25.171	0.725	1.00	52.55	L111 C
ATOM	988	C	VAL A 139	-7.561	26.549	1.370	1.00	53.32	L111 C
ATOM	989	O	VAL A 139	-6.578	27.164	1.782	1.00	54.50	L111 O
ATOM	990	CB	VAL A 139	-7.144	24.122	1.838	1.00	47.09	L111 C
ATOM	991	CG1	VAL A 139	-7.486	22.741	1.332	1.00	46.28	L111 C
ATOM	992	CG2	VAL A 139	-5.689	24.171	2.281	1.00	54.07	L111 C
ATOM	993	N	VAL A 140	-8.799	27.028	1.454	1.00	57.53	L111 N
ATOM	994	CA	VAL A 140	-9.076	28.334	2.045	1.00	58.40	L111 C
ATOM	995	C	VAL A 140	-10.295	28.298	2.970	1.00	64.90	L111 C
ATOM	996	O	VAL A 140	-11.243	27.540	2.674	1.00	63.16	L111 O
ATOM	997	CB	VAL A 140	-9.321	29.394	0.950	1.00	56.76	L111 C
ATOM	998	CG1	VAL A 140	-8.207	29.343	-0.082	1.00	48.47	L111 C
ATOM	999	CG2	VAL A 140	-10.667	29.156	0.288	1.00	56.93	L111 C
ATOM	1000	OXT	VAL A 140	-10.290	29.036	3.980	1.00	72.53	L111 O
TER	1001		VAL A 140						
ATOM	1002	N	LYS B 71	-21.043	-5.854	-42.905	1.00	63.31	L112 N
ATOM	1003	CA	LYS B 71	-20.335	-6.681	-43.925	1.00	62.12	L112 C
ATOM	1004	C	LYS B 71	-20.331	-8.162	-43.563	1.00	64.08	L112 C
ATOM	1005	O	LYS B 71	-20.688	-8.546	-42.446	1.00	64.38	L112 O
ATOM	1006	CB	LYS B 71	-18.892	-6.202	-44.080	1.00	58.09	L112 C
ATOM	1007	CG	LYS B 71	-18.753	-4.928	-44.883	1.00	57.55	L112 C
ATOM	1008	CD	LYS B 71	-17.414	-4.877	-45.584	1.00	59.51	L112 C
ATOM	1009	CE	LYS B 71	-17.502	-4.091	-46.883	1.00	73.52	L112 C
ATOM	1010	NZ	LYS B 71	-16.276	-3.277	-47.136	1.00	74.38	L112 N
ATOM	1011	N	THR B 72	-19.922	-8.992	-44.517	1.00	60.82	L112 N
ATOM	1012	CA	THR B 72	-19.866	-10.432	-44.305	1.00	53.90	L112 C
ATOM	1013	C	THR B 72	-18.602	-10.793	-43.534	1.00	45.75	L112 C
ATOM	1014	O	THR B 72	-17.573	-10.123	-43.661	1.00	42.26	L112 O
ATOM	1015	CB	THR B 72	-19.881	-11.190	-45.647	1.00	54.39	L112 C
ATOM	1016	OG1	THR B 72	-20.261	-10.291	-46.695	1.00	53.11	L112 O
ATOM	1017	CG2	THR B 72	-20.877	-12.340	-45.603	1.00	54.95	L112 C
ATOM	1018	N	PRO B 73	-18.664	-11.860	-42.721	1.00	37.48	L112 N
ATOM	1019	CA	PRO B 73	-17.507	-12.290	-41.935	1.00	34.20	L112 C
ATOM	1020	C	PRO B 73	-16.302	-12.518	-42.828	1.00	36.67	L112 C
ATOM	1021	O	PRO B 73	-16.441	-12.715	-44.034	1.00	42.32	L112 O
ATOM	1022	CB	PRO B 73	-17.977	-13.578	-41.271	1.00	35.95	L112 C
ATOM	1023	CG	PRO B 73	-19.465	-13.478	-41.261	1.00	38.50	L112 C
ATOM	1024	CD	PRO B 73	-19.831	-12.733	-42.504	1.00	38.65	L112 C
ATOM	1025	N	PRO B 74	-15.097	-12.500	-42.247	1.00	30.98	L112 N
ATOM	1026	CA	PRO B 74	-13.896	-12.712	-43.056	1.00	29.22	L112 C
ATOM	1027	C	PRO B 74	-13.949	-14.071	-43.737	1.00	30.46	L112 C

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ATOM 1028	O	PRO B 74	-14.664 -14.971 -43.292	1.00 34.58	L112 O
ATOM 1029	CB	PRO B 74	-12.755 -12.620 -42.042	1.00 26.89	L112 C
ATOM 1030	CG	PRO B 74	-13.334 -11.909 -40.876	1.00 16.14	L112 C
ATOM 1031	CD	PRO B 74	-14.773 -12.302 -40.828	1.00 24.82	L112 C
ATOM 1032	N	ALA B 75	-13.196 -14.217 -44.819	1.00 26.98	L112 N
ATOM 1033	CA	ALA B 75	-13.162 -15.472 -45.540	1.00 21.93	L112 C
ATOM 1034	C	ALA B 75	-12.623 -16.534 -44.597	1.00 29.69	L112 C
ATOM 1035	O	ALA B 75	-13.190 -17.619 -44.481	1.00 33.14	L112 O
ATOM 1036	CB	ALA B 75	-12.264 -15.346 -46.760	1.00 29.99	L112 C
ATOM 1037	N	SER B 76	-11.530 -16.210 -43.912	1.00 29.96	L112 N
ATOM 1038	CA	SER B 76	-10.911 -17.143 -42.978	1.00 31.14	L112 C
ATOM 1039	C	SER B 76	-11.908 -17.595 -41.918	1.00 36.21	L112 C
ATOM 1040	O	SER B 76	-11.922 -18.760 -41.517	1.00 38.58	L112 O
ATOM 1041	CB	SER B 76	-9.700 -16.496 -42.305	1.00 28.76	L112 C
ATOM 1042	OG	SER B 76	-10.103 -15.622 -41.266	1.00 33.61	L112 O
ATOM 1043	N	PHE B 77	-12.748 -16.674 -41.465	1.00 35.12	L112 N
ATOM 1044	CA	PHE B 77	-13.731 -17.018 -40.457	1.00 36.06	L112 C
ATOM 1045	C	PHE B 77	-14.684 -18.047 -41.025	1.00 38.63	L112 C
ATOM 1046	O	PHE B 77	-14.874 -19.116 -40.448	1.00 43.61	L112 O
ATOM 1047	CB	PHE B 77	-14.518 -15.787 -40.025	1.00 44.62	L112 C
ATOM 1048	CG	PHE B 77	-15.644 -16.097 -39.080	1.00 47.58	L112 C
ATOM 1049	CD1	PHE B 77	-15.388 -16.347 -37.733	1.00 44.42	L112 C
ATOM 1050	CD2	PHE B 77	-16.959 -16.151 -39.536	1.00 44.81	L112 C
ATOM 1051	CE1	PHE B 77	-16.424 -16.646 -36.855	1.00 40.74	L112 C
ATOM 1052	CE2	PHE B 77	-18.003 -16.449 -38.667	1.00 42.72	L112 C
ATOM 1053	CZ	PHE B 77	-17.736 -16.697 -37.322	1.00 44.82	L112 C
ATOM 1054	N	LEU B 78	-15.288 -17.719 -42.161	1.00 37.81	L112 N
ATOM 1055	CA	LEU B 78	-16.228 -18.625 -42.810	1.00 36.34	L112 C
ATOM 1056	C	LEU B 78	-15.574 -19.970 -43.100	1.00 31.89	L112 C
ATOM 1057	O	LEU B 78	-16.204 -21.017 -42.980	1.00 35.90	L112 O
ATOM 1058	CB	LEU B 78	-16.743 -17.998 -44.105	1.00 34.71	L112 C
ATOM 1059	CG	LEU B 78	-17.603 -16.750 -43.895	1.00 33.80	L112 C
ATOM 1060	CD1	LEU B 78	-18.030 -16.182 -45.238	1.00 29.39	L112 C
ATOM 1061	CD2	LEU B 78	-18.817 -17.113 -43.052	1.00 29.74	L112 C
ATOM 1062	N	LEU B 79	-14.302 -19.936 -43.474	1.00 26.28	L112 N
ATOM 1063	CA	LEU B 79	-13.566 -21.153 -43.765	1.00 31.61	L112 C
ATOM 1064	C	LEU B 79	-13.420 -22.002 -42.498	1.00 39.25	L112 C
ATOM 1065	O	LEU B 79	-13.727 -23.194 -42.508	1.00 40.69	L112 O
ATOM 1066	CB	LEU B 79	-12.192 -20.799 -44.344	1.00 31.36	L112 C
ATOM 1067	CG	LEU B 79	-12.229 -20.369 -45.816	1.00 25.54	L112 C
ATOM 1068	CD1	LEU B 79	-10.852 -19.971 -46.314	1.00 21.73	L112 C
ATOM 1069	CD2	LEU B 79	-12.763 -21.520 -46.635	1.00 23.94	L112 C
ATOM 1070	N	LYS B 80	-12.960 -21.384 -41.411	1.00 44.27	L112 N
ATOM 1071	CA	LYS B 80	-12.794 -22.078 -40.131	1.00 39.57	L112 C
ATOM 1072	C	LYS B 80	-14.075 -22.822 -39.785	1.00 35.79	L112 C

ATOM	1073	O	LYS B 80	-14.049	-23.993	-39.418	1.00	37.45	L112 O
ATOM	1074	CB	LYS B 80	-12.500	-21.077	-39.008	1.00	44.26	L112 C
ATOM	1075	CG	LYS B 80	-11.028	-20.840	-38.710	1.00	46.47	L112 C
ATOM	1076	CD	LYS B 80	-10.839	-19.591	-37.850	1.00	45.33	L112 C
ATOM	1077	CE	LYS B 80	-9.377	-19.388	-37.474	1.00	50.24	L112 C
ATOM	1078	NZ	LYS B 80	-9.071	-17.963	-37.174	1.00	50.61	L112 N
ATOM	1079	N	LYS B 81	-15.197	-22.122	-39.907	1.00	34.23	L112 N
ATOM	1080	CA	LYS B 81	-16.508	-22.682	-39.609	1.00	39.48	L112 C
ATOM	1081	C	LYS B 81	-16.845	-23.880	-40.485	1.00	42.52	L112 C
ATOM	1082	O	LYS B 81	-17.253	-24.929	-39.991	1.00	49.15	L112 O
ATOM	1083	CB	LYS B 81	-17.580	-21.607	-39.787	1.00	41.03	L112 C
ATOM	1084	CG	LYS B 81	-18.306	-21.234	-38.510	1.00	52.41	L112 C
ATOM	1085	CD	LYS B 81	-19.812	-21.200	-38.730	1.00	68.51	L112 C
ATOM	1086	CE	LYS B 81	-20.234	-19.983	-39.549	1.00	73.66	L112 C
ATOM	1087	NZ	LYS B 81	-20.152	-20.217	-41.023	1.00	71.12	L112 N
ATOM	1088	N	ALA B 82	-16.678	-23.722	-41.792	1.00	45.81	L112 N
ATOM	1089	CA	ALA B 82	-16.979	-24.800	-42.725	1.00	44.23	L112 C
ATOM	1090	C	ALA B 82	-16.154	-26.049	-42.431	1.00	40.55	L112 C
ATOM	1091	O	ALA B 82	-16.662	-27.165	-42.503	1.00	39.77	L112 O
ATOM	1092	CB	ALA B 82	-16.729	-24.336	-44.149	1.00	42.43	L112 C
ATOM	1093	N	ALA B 83	-14.882	-25.855	-42.101	1.00	35.34	L112 N
ATOM	1094	CA	ALA B 83	-13.990	-26.967	-41.807	1.00	33.10	L112 C
ATOM	1095	C	ALA B 83	-14.259	-27.559	-40.431	1.00	40.90	L112 C
ATOM	1096	O	ALA B 83	-13.797	-28.659	-40.123	1.00	42.00	L112 O
ATOM	1097	CB	ALA B 83	-12.544	-26.514	-41.898	1.00	30.83	L112 C
ATOM	1098	N	GLY B 84	-15.000	-26.823	-39.605	1.00	43.37	L112 N
ATOM	1099	CA	GLY B 84	-15.320	-27.292	-38.267	1.00	40.61	L112 C
ATOM	1100	C	GLY B 84	-14.164	-27.194	-37.287	1.00	41.90	L112 C
ATOM	1101	O	GLY B 84	-14.061	-27.997	-36.361	1.00	45.63	L112 O
ATOM	1102	N	ILE B 85	-13.283	-26.222	-37.495	1.00	40.72	L112 N
ATOM	1103	CA	ILE B 85	-12.141	-26.025	-36.612	1.00	39.23	L112 C
ATOM	1104	C	ILE B 85	-12.283	-24.664	-35.944	1.00	44.21	L112 C
ATOM	1105	O	ILE B 85	-13.168	-23.884	-36.304	1.00	48.06	L112 O
ATOM	1106	CB	ILE B 85	-10.801	-26.081	-37.388	1.00	34.91	L112 C
ATOM	1107	CG1	ILE B 85	-10.738	-24.959	-38.423	1.00	34.57	L112 C
ATOM	1108	CG2	ILE B 85	-10.657	-27.425	-38.076	1.00	33.20	L112 C
ATOM	1109	CD1	ILE B 85	-9.477	-24.973	-39.258	1.00	32.16	L112 C
ATOM	1110	N	GLU B 86	-11.422	-24.380	-34.972	1.00	45.20	L112 N
ATOM	1111	CA	GLU B 86	-11.484	-23.108	-34.266	1.00	43.68	L112 C
ATOM	1112	C	GLU B 86	-10.261	-22.245	-34.544	1.00	41.68	L112 C
ATOM	1113	O	GLU B 86	-10.258	-21.049	-34.257	1.00	47.94	L112 O
ATOM	1114	CB	GLU B 86	-11.632	-23.347	-32.760	1.00	46.15	L112 C
ATOM	1115	CG	GLU B 86	-10.322	-23.581	-32.020	1.00	65.68	L112 C
ATOM	1116	CD	GLU B 86	-10.394	-23.163	-30.561	1.00	76.24	L112 C
ATOM	1117	OE1	GLU B 86	-11.440	-23.417	-29.922	1.00	79.61	L112 O

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ATOM	1118	OE2 GLU B 86	-9.409 -22.580 -30.054	1.00 77.24	L112 O
ATOM	1119	N LYS B 87	-9.222 -22.850 -35.103	1.00 33.13	L112 N
ATOM	1120	CA LYS B 87	-8.011 -22.109 -35.416	1.00 40.07	L112 C
ATOM	1121	C LYS B 87	-7.423 -22.570 -36.741	1.00 40.26	L112 C
ATOM	1122	O LYS B 87	-7.610 -23.712 -37.150	1.00 46.66	L112 O
ATOM	1123	CB LYS B 87	-6.973 -22.293 -34.306	1.00 43.57	L112 C
ATOM	1124	CG LYS B 87	-7.240 -21.468 -33.057	1.00 57.30	L112 C
ATOM	1125	CD LYS B 87	-6.210 -21.759 -31.970	1.00 60.56	L112 C
ATOM	1126	CE LYS B 87	-5.750 -20.483 -31.279	1.00 59.04	L112 C
ATOM	1127	NZ LYS B 87	-6.112 -19.261 -32.054	1.00 64.31	L112 N
ATOM	1128	N GLY B 88	-6.725 -21.671 -37.418	1.00 34.46	L112 N
ATOM	1129	CA GLY B 88	-6.110 -22.038 -38.672	1.00 33.11	L112 C
ATOM	1130	C GLY B 88	-4.818 -22.742 -38.333	1.00 31.13	L112 C
ATOM	1131	O GLY B 88	-4.402 -22.747 -37.180	1.00 34.45	L112 O
ATOM	1132	N SER B 89	-4.183 -23.345 -39.325	1.00 31.44	L112 N
ATOM	1133	CA SER B 89	-2.935 -24.043 -39.093	1.00 29.45	L112 C
ATOM	1134	C SER B 89	-1.871 -23.027 -38.709	1.00 37.64	L112 C
ATOM	1135	O SER B 89	-1.904 -21.889 -39.167	1.00 39.44	L112 O
ATOM	1136	CB SER B 89	-2.519 -24.789 -40.357	1.00 30.04	L112 C
ATOM	1137	OG SER B 89	-1.138 -25.097 -40.339	1.00 30.69	L112 O
ATOM	1138	N SER B 90	-0.932 -23.437 -37.863	1.00 34.79	L112 N
ATOM	1139	CA SER B 90	0.145 -22.556 -37.434	1.00 36.73	L112 C
ATOM	1140	C SER B 90	1.250 -22.593 -38.480	1.00 37.59	L112 C
ATOM	1141	O SER B 90	2.173 -21.778 -38.474	1.00 38.46	L112 O
ATOM	1142	CB SER B 90	0.698 -23.023 -36.092	1.00 42.80	L112 C
ATOM	1143	OG SER B 90	1.368 -24.265 -36.234	1.00 57.39	L112 O
ATOM	1144	N GLU B 91	1.153 -23.565 -39.373	1.00 40.27	L112 N
ATOM	1145	CA GLU B 91	2.122 -23.726 -40.445	1.00 44.62	L112 C
ATOM	1146	C GLU B 91	1.352 -24.125 -41.697	1.00 42.72	L112 C
ATOM	1147	O GLU B 91	1.316 -25.295 -42.067	1.00 49.13	L112 O
ATOM	1148	CB GLU B 91	3.135 -24.812 -40.085	1.00 47.12	L112 C
ATOM	1149	CG GLU B 91	4.520 -24.289 -39.768	1.00 58.48	L112 C
ATOM	1150	CD GLU B 91	5.431 -25.364 -39.208	1.00 65.15	L112 C
ATOM	1151	OE1 GLU B 91	5.935 -26.197 -39.997	1.00 68.92	L112 O
ATOM	1152	OE2 GLU B 91	5.643 -25.374 -37.976	1.00 74.00	L112 O
ATOM	1153	N PRO B 92	0.699 -23.154 -42.352	1.00 40.19	L112 N
ATOM	1154	CA PRO B 92	-0.071 -23.435 -43.566	1.00 40.89	L112 C
ATOM	1155	C PRO B 92	0.736 -24.213 -44.603	1.00 42.71	L112 C
ATOM	1156	O PRO B 92	1.955 -24.035 -44.720	1.00 32.77	L112 O
ATOM	1157	CB PRO B 92	-0.467 -22.049 -44.062	1.00 43.77	L112 C
ATOM	1158	CG PRO B 92	-0.489 -21.217 -42.818	1.00 42.90	L112 C
ATOM	1159	CD PRO B 92	0.642 -21.729 -41.987	1.00 35.83	L112 C
ATOM	1160	N LYS B 93	0.043 -25.074 -45.346	1.00 45.71	L112 N
ATOM	1161	CA LYS B 93	0.656 -25.905 -46.380	1.00 42.76	L112 C
ATOM	1162	C LYS B 93	1.431 -27.073 -45.773	1.00 42.07	L112 C

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ATOM	1208	N	LYS B 99	-10.373	-29.402	-43.627	1.00	29.50	L112 N
ATOM	1209	CA	LYS B 99	-10.634	-29.516	-45.046	1.00	32.51	L112 C
ATOM	1210	C	LYS B 99	-12.080	-29.187	-45.374	1.00	36.44	L112 C
ATOM	1211	O	LYS B 99	-12.976	-29.448	-44.575	1.00	35.95	L112 O
ATOM	1212	CB	LYS B 99	-10.315	-30.937	-45.507	1.00	39.97	L112 C
ATOM	1213	CG	LYS B 99	-10.933	-32.025	-44.639	1.00	41.83	L112 C
ATOM	1214	CD	LYS B 99	-11.335	-33.237	-45.469	1.00	51.41	L112 C
ATOM	1215	CE	LYS B 99	-10.486	-34.453	-45.134	1.00	53.02	L112 C
ATOM	1216	NZ	LYS B 99	-11.298	-35.553	-44.538	1.00	66.17	L112 N
ATOM	1217	N	VAL B 100	-12.298	-28.609	-46.555	1.00	40.79	L112 N
ATOM	1218	CA	VAL B 100	-13.642	-28.263	-47.010	1.00	40.95	L112 C
ATOM	1219	C	VAL B 100	-13.871	-28.788	-48.419	1.00	41.23	L112 C
ATOM	1220	O	VAL B 100	-12.927	-28.948	-49.199	1.00	37.76	L112 O
ATOM	1221	CB	VAL B 100	-13.877	-26.742	-47.033	1.00	42.14	L112 C
ATOM	1222	CG1	VAL B 100	-14.062	-26.228	-45.623	1.00	47.48	L112 C
ATOM	1223	CG2	VAL B 100	-12.714	-26.049	-47.719	1.00	46.52	L112 C
ATOM	1224	N	THR B 101	-15.134	-29.054	-48.737	1.00	43.68	L112 N
ATOM	1225	CA	THR B 101	-15.505	-29.556	-50.052	1.00	44.90	L112 C
ATOM	1226	C	THR B 101	-15.572	-28.401	-51.030	1.00	46.97	L112 C
ATOM	1227	O	THR B 101	-15.847	-27.266	-50.641	1.00	49.23	L112 O
ATOM	1228	CB	THR B 101	-16.882	-30.228	-50.037	1.00	44.59	L112 C
ATOM	1229	OG1	THR B 101	-17.875	-29.262	-49.670	1.00	47.42	L112 O
ATOM	1230	CG2	THR B 101	-16.904	-31.382	-49.050	1.00	37.18	L112 C
ATOM	1231	N	ARG B 102	-15.319	-28.692	-52.301	1.00	47.23	L112 N
ATOM	1232	CA	ARG B 102	-15.376	-27.664	-53.324	1.00	42.99	L112 C
ATOM	1233	C	ARG B 102	-16.760	-27.046	-53.255	1.00	39.27	L112 C
ATOM	1234	O	ARG B 102	-16.947	-25.888	-53.609	1.00	51.83	L112 O
ATOM	1235	CB	ARG B 102	-15.140	-28.272	-54.708	1.00	50.12	L112 C
ATOM	1236	CG	ARG B 102	-14.295	-27.405	-55.639	1.00	58.67	L112 C
ATOM	1237	CD	ARG B 102	-12.884	-27.964	-55.821	1.00	61.68	L112 C
ATOM	1238	NE	ARG B 102	-12.827	-29.413	-55.632	1.00	63.94	L112 N
ATOM	1239	CZ	ARG B 102	-11.703	-30.124	-55.623	1.00	67.71	L112 C
ATOM	1240	NH1	ARG B 102	-10.534	-29.517	-55.793	1.00	66.40	L112 N
ATOM	1241	NH2	ARG B 102	-11.747	-31.442	-55.443	1.00	60.88	L112 N
ATOM	1242	N	LYS B 103	-17.730	-27.823	-52.786	1.00	37.67	L112 N
ATOM	1243	CA	LYS B 103	-19.096	-27.333	-52.664	1.00	41.92	L112 C
ATOM	1244	C	LYS B 103	-19.160	-26.308	-51.547	1.00	44.83	L112 C
ATOM	1245	O	LYS B 103	-19.856	-25.298	-51.649	1.00	49.24	L112 O
ATOM	1246	CB	LYS B 103	-20.056	-28.483	-52.354	1.00	49.35	L112 C
ATOM	1247	CG	LYS B 103	-21.265	-28.079	-51.510	1.00	57.47	L112 C
ATOM	1248	CD	LYS B 103	-22.244	-27.221	-52.298	1.00	66.45	L112 C
ATOM	1249	CE	LYS B 103	-23.683	-27.670	-52.075	1.00	76.17	L112 C
ATOM	1250	NZ	LYS B 103	-24.099	-27.557	-50.645	1.00	75.72	L112 N
ATOM	1251	N	GLN B 104	-18.434	-26.578	-50.471	1.00	44.97	L112 N
ATOM	1252	CA	GLN B 104	-18.412	-25.662	-49.347	1.00	43.50	L112 C

ATOM	1253	C	GLN B 104	-17.766	-24.359	-49.796	1.00	37.68	L112 C
ATOM	1254	O	GLN B 104	-18.268	-23.277	-49.500	1.00	38.95	L112 O
ATOM	1255	CB	GLN B 104	-17.640	-26.279	-48.181	1.00	47.34	L112 C
ATOM	1256	CG	GLN B 104	-18.442	-27.328	-47.425	1.00	42.38	L112 C
ATOM	1257	CD	GLN B 104	-17.693	-27.890	-46.237	1.00	42.53	L112 C
ATOM	1258	OE1	GLN B 104	-16.603	-28.446	-46.380	1.00	35.56	L112 O
ATOM	1259	NE2	GLN B 104	-18.275	-27.745	-45.050	1.00	36.61	L112 N
ATOM	1260	N	ILE B 105	-16.660	-24.471	-50.525	1.00	30.76	L112 N
ATOM	1261	CA	ILE B 105	-15.962	-23.296	-51.026	1.00	35.17	L112 C
ATOM	1262	C	ILE B 105	-16.931	-22.427	-51.811	1.00	39.38	L112 C
ATOM	1263	O	ILE B 105	-16.880	-21.202	-51.736	1.00	44.28	L112 O
ATOM	1264	CB	ILE B 105	-14.808	-23.678	-51.962	1.00	26.23	L112 C
ATOM	1265	CG1	ILE B 105	-13.674	-24.314	-51.159	1.00	35.32	L112 C
ATOM	1266	CG2	ILE B 105	-14.320	-22.442	-52.714	1.00	30.76	L112 C
ATOM	1267	CD1	ILE B 105	-12.778	-23.317	-50.444	1.00	30.65	L112 C
ATOM	1268	N	GLU B 106	-17.815	-23.074	-52.563	1.00	44.23	L112 N
ATOM	1269	CA	GLU B 106	-18.800	-22.367	-53.366	1.00	48.57	L112 C
ATOM	1270	C	GLU B 106	-19.776	-21.590	-52.488	1.00	50.45	L112 C
ATOM	1271	O	GLU B 106	-20.083	-20.430	-52.769	1.00	52.09	L112 O
ATOM	1272	CB	GLU B 106	-19.563	-23.358	-54.249	1.00	56.57	L112 C
ATOM	1273	CG	GLU B 106	-20.814	-22.786	-54.920	1.00	65.87	L112 C
ATOM	1274	CD	GLU B 106	-21.335	-23.664	-56.053	1.00	68.27	L112 C
ATOM	1275	OE1	GLU B 106	-20.505	-24.254	-56.781	1.00	62.09	L112 O
ATOM	1276	OE2	GLU B 106	-22.573	-23.762	-56.214	1.00	66.69	L112 O
ATOM	1277	N	GLU B 107	-20.258	-22.222	-51.422	1.00	48.38	L112 N
ATOM	1278	CA	GLU B 107	-21.204	-21.567	-50.523	1.00	50.26	L112 C
ATOM	1279	C	GLU B 107	-20.610	-20.317	-49.890	1.00	50.25	L112 C
ATOM	1280	O	GLU B 107	-21.311	-19.332	-49.661	1.00	52.98	L112 O
ATOM	1281	CB	GLU B 107	-21.648	-22.527	-49.425	1.00	52.51	L112 C
ATOM	1282	CG	GLU B 107	-22.481	-23.685	-49.921	1.00	72.08	L112 C
ATOM	1283	CD	GLU B 107	-22.371	-24.896	-49.016	1.00	86.41	L112 C
ATOM	1284	OE1	GLU B 107	-21.249	-25.188	-48.545	1.00	91.57	L112 O
ATOM	1285	OE2	GLU B 107	-23.405	-25.554	-48.772	1.00	92.70	L112 O
ATOM	1286	N	ILE B 108	-19.315	-20.355	-49.602	1.00	46.38	L112 N
ATOM	1287	CA	ILE B 108	-18.667	-19.206	-48.999	1.00	43.09	L112 C
ATOM	1288	C	ILE B 108	-18.525	-18.099	-50.030	1.00	42.47	L112 C
ATOM	1289	O	ILE B 108	-18.815	-16.937	-49.748	1.00	47.10	L112 O
ATOM	1290	CB	ILE B 108	-17.272	-19.565	-48.449	1.00	42.76	L112 C
ATOM	1291	CG1	ILE B 108	-17.407	-20.613	-47.345	1.00	35.09	L112 C
ATOM	1292	CG2	ILE B 108	-16.592	-18.317	-47.891	1.00	31.13	L112 C
ATOM	1293	CD1	ILE B 108	-16.084	-21.041	-46.747	1.00	41.11	L112 C
ATOM	1294	N	ALA B 109	-18.081	-18.464	-51.229	1.00	38.62	L112 N
ATOM	1295	CA	ALA B 109	-17.900	-17.486	-52.293	1.00	38.24	L112 C
ATOM	1296	C	ALA B 109	-19.208	-16.761	-52.539	1.00	37.79	L112 C
ATOM	1297	O	ALA B 109	-19.222	-15.562	-52.807	1.00	37.18	L112 O

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ATOM 1298 CB ALA B 109	-17.436 -18.172 -53.562	1.00 38.10	L112 C
ATOM 1299 N LYS B 110	-20.309 -17.497 -52.437	1.00 38.29	L112 N
ATOM 1300 CA LYS B 110	-21.626 -16.917 -52.647	1.00 42.58	L112 C
ATOM 1301 C LYS B 110	-21.945 -15.951 -51.518	1.00 45.99	L112 C
ATOM 1302 O LYS B 110	-22.468 -14.858 -51.747	1.00 55.26	L112 O
ATOM 1303 CB LYS B 110	-22.689 -18.016 -52.702	1.00 39.40	L112 C
ATOM 1304 CG LYS B 110	-22.558 -18.947 -53.898	1.00 51.26	L112 C
ATOM 1305 CD LYS B 110	-23.911 -19.512 -54.329	1.00 60.46	L112 C
ATOM 1306 CE LYS B 110	-23.897 -19.968 -55.790	1.00 63.75	L112 C
ATOM 1307 NZ LYS B 110	-24.464 -21.340 -55.985	1.00 64.25	L112 N
ATOM 1308 N THR B 111	-21.620 -16.357 -50.297	1.00 40.79	L112 N
ATOM 1309 CA THR B 111	-21.876 -15.527 -49.134	1.00 38.24	L112 C
ATOM 1310 C THR B 111	-21.088 -14.231 -49.196	1.00 42.37	L112 C
ATOM 1311 O THR B 111	-21.644 -13.152 -48.998	1.00 48.64	L112 O
ATOM 1312 CB THR B 111	-21.490 -16.256 -47.845	1.00 42.62	L112 C
ATOM 1313 OG1 THR B 111	-22.140 -17.531 -47.812	1.00 49.22	L112 O
ATOM 1314 CG2 THR B 111	-21.899 -15.441 -46.630	1.00 41.08	L112 C
ATOM 1315 N LYS B 112	-19.794 -14.346 -49.479	1.00 41.09	L112 N
ATOM 1316 CA LYS B 112	-18.900 -13.194 -49.544	1.00 38.50	L112 C
ATOM 1317 C LYS B 112	-18.910 -12.449 -50.879	1.00 43.09	L112 C
ATOM 1318 O LYS B 112	-18.246 -11.424 -51.018	1.00 40.13	L112 O
ATOM 1319 CB LYS B 112	-17.467 -13.640 -49.240	1.00 35.11	L112 C
ATOM 1320 CG LYS B 112	-17.124 -13.715 -47.764	1.00 33.43	L112 C
ATOM 1321 CD LYS B 112	-16.011 -12.742 -47.409	1.00 29.28	L112 C
ATOM 1322 CE LYS B 112	-16.567 -11.530 -46.680	1.00 35.42	L112 C
ATOM 1323 NZ LYS B 112	-15.524 -10.509 -46.385	1.00 31.34	L112 N
ATOM 1324 N MET B 113	-19.654 -12.957 -51.857	1.00 50.88	L112 N
ATOM 1325 CA MET B 113	-19.709 -12.331 -53.180	1.00 51.11	L112 C
ATOM 1326 C MET B 113	-19.879 -10.807 -53.156	1.00 49.15	L112 C
ATOM 1327 O MET B 113	-19.130 -10.081 -53.813	1.00 50.15	L112 O
ATOM 1328 CB MET B 113	-20.824 -12.962 -54.022	1.00 51.18	L112 C
ATOM 1329 CG MET B 113	-20.717 -12.654 -55.515	1.00 47.98	L112 C
ATOM 1330 SD MET B 113	-19.263 -13.400 -56.298	1.00 49.73	L112 S
ATOM 1331 CE MET B 113	-18.549 -11.969 -57.088	1.00 52.43	L112 C
ATOM 1332 N PRO B 114	-20.870 -10.301 -52.409	1.00 42.31	L112 N
ATOM 1333 CA PRO B 114	-21.051 -8.849 -52.369	1.00 41.88	L112 C
ATOM 1334 C PRO B 114	-19.781 -8.079 -51.997	1.00 44.88	L112 C
ATOM 1335 O PRO B 114	-19.589 -6.945 -52.439	1.00 51.97	L112 O
ATOM 1336 CB PRO B 114	-22.171 -8.646 -51.345	1.00 38.22	L112 C
ATOM 1337 CG PRO B 114	-22.290 -9.946 -50.621	1.00 43.79	L112 C
ATOM 1338 CD PRO B 114	-21.870 -11.000 -51.588	1.00 46.66	L112 C
ATOM 1339 N ASP B 115	-18.912 -8.690 -51.197	1.00 46.07	L112 N
ATOM 1340 CA ASP B 115	-17.673 -8.030 -50.785	1.00 45.61	L112 C
ATOM 1341 C ASP B 115	-16.506 -8.353 -51.709	1.00 42.88	L112 C
ATOM 1342 O ASP B 115	-15.435 -7.758 -51.598	1.00 47.89	L112 O

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ATOM	1343	CB	ASP B 115	-17.292	-8.429	-49.355	1.00	51.51	L112 C
ATOM	1344	CG	ASP B 115	-18.431	-8.252	-48.368	1.00	50.88	L112 C
ATOM	1345	OD1	ASP B 115	-19.514	-7.787	-48.779	1.00	57.98	L112 O
ATOM	1346	OD2	ASP B 115	-18.240	-8.582	-47.178	1.00	59.37	L112 O
ATOM	1347	N	LEU B 116	-16.713	-9.298	-52.618	1.00	40.70	L112 N
ATOM	1348	CA	LEU B 116	-15.669	-9.698	-53.553	1.00	37.46	L112 C
ATOM	1349	C	LEU B 116	-15.698	-8.849	-54.819	1.00	37.00	L112 C
ATOM	1350	O	LEU B 116	-16.757	-8.385	-55.242	1.00	38.81	L112 O
ATOM	1351	CB	LEU B 116	-15.851	-11.169	-53.939	1.00	40.60	L112 C
ATOM	1352	CG	LEU B 116	-15.289	-12.293	-53.065	1.00	35.62	L112 C
ATOM	1353	CD1	LEU B 116	-14.872	-11.765	-51.707	1.00	42.51	L112 C
ATOM	1354	CD2	LEU B 116	-16.347	-13.368	-52.923	1.00	33.28	L112 C
ATOM	1355	N	ASN B 117	-14.535	-8.653	-55.429	1.00	32.39	L112 N
ATOM	1356	CA	ASN B 117	-14.467	-7.886	-56.662	1.00	32.20	L112 C
ATOM	1357	C	ASN B 117	-14.427	-8.835	-57.867	1.00	37.64	L112 C
ATOM	1358	O	ASN B 117	-14.193	-8.415	-59.001	1.00	35.01	L112 O
ATOM	1359	CB	ASN B 117	-13.235	-6.984	-56.655	1.00	24.31	L112 C
ATOM	1360	CG	ASN B 117	-11.952	-7.762	-56.709	1.00	29.72	L112 C
ATOM	1361	OD1	ASN B 117	-11.914	-8.941	-56.354	1.00	32.78	L112 O
ATOM	1362	ND2	ASN B 117	-10.883	-7.110	-57.154	1.00	25.55	L112 N
ATOM	1363	N	ALA B 118	-14.662	-10.117	-57.608	1.00	39.75	L112 N
ATOM	1364	CA	ALA B 118	-14.665	-11.130	-58.656	1.00	41.80	L112 C
ATOM	1365	C	ALA B 118	-15.862	-10.910	-59.567	1.00	45.30	L112 C
ATOM	1366	O	ALA B 118	-16.863	-10.330	-59.156	1.00	53.58	L112 O
ATOM	1367	CB	ALA B 118	-14.734	-12.512	-58.043	1.00	30.65	L112 C
ATOM	1368	N	ASN B 119	-15.760	-11.381	-60.804	1.00	46.03	L112 N
ATOM	1369	CA	ASN B 119	-16.840	-11.216	-61.766	1.00	48.46	L112 C
ATOM	1370	C	ASN B 119	-17.574	-12.516	-62.081	1.00	50.16	L112 C
ATOM	1371	O	ASN B 119	-18.557	-12.512	-62.817	1.00	55.94	L112 O
ATOM	1372	CB	ASN B 119	-16.287	-10.625	-63.061	1.00	49.26	L112 C
ATOM	1373	CG	ASN B 119	-16.023	-9.137	-62.958	1.00	50.05	L112 C
ATOM	1374	OD1	ASN B 119	-16.747	-8.407	-62.269	1.00	48.95	L112 O
ATOM	1375	ND2	ASN B 119	-14.981	-8.674	-63.646	1.00	48.05	L112 N
ATOM	1376	N	SER B 120	-17.096	-13.624	-61.527	1.00	51.92	L112 N
ATOM	1377	CA	SER B 120	-17.711	-14.924	-61.771	1.00	47.70	L112 C
ATOM	1378	C	SER B 120	-17.599	-15.828	-60.555	1.00	50.21	L112 C
ATOM	1379	O	SER B 120	-16.614	-15.770	-59.823	1.00	58.54	L112 O
ATOM	1380	CB	SER B 120	-17.034	-15.609	-62.964	1.00	46.48	L112 C
ATOM	1381	OG	SER B 120	-15.617	-15.558	-62.866	1.00	29.64	L112 O
ATOM	1382	N	LEU B 121	-18.607	-16.670	-60.346	1.00	49.76	L112 N
ATOM	1383	CA	LEU B 121	-18.591	-17.600	-59.225	1.00	44.29	L112 C
ATOM	1384	C	LEU B 121	-17.276	-18.369	-59.261	1.00	42.13	L112 C
ATOM	1385	O	LEU B 121	-16.669	-18.628	-58.229	1.00	45.70	L112 O
ATOM	1386	CB	LEU B 121	-19.760	-18.578	-59.327	1.00	41.45	L112 C
ATOM	1387	CG	LEU B 121	-19.784	-19.676	-58.262	1.00	41.89	L112 C





ATOM	1433	CD1 ILE B 127	-12.047 -12.810 -55.482	1.00 31.68	L112 C
ATOM	1434	N ILE B 128	-11.608 -17.439 -52.396	1.00 20.75	L112 N
ATOM	1435	CA ILE B 128	-11.731 -18.104 -51.111	1.00 18.60	L112 C
ATOM	1436	C ILE B 128	-10.637 -19.152 -50.969	1.00 23.21	L112 C
ATOM	1437	O ILE B 128	-9.936 -19.202 -49.960	1.00 34.11	L112 O
ATOM	1438	CB ILE B 128	-13.084 -18.796 -50.975	1.00 17.63	L112 C
ATOM	1439	CG1 ILE B 128	-14.208 -17.807 -51.280	1.00 17.94	L112 C
ATOM	1440	CG2 ILE B 128	-13.236 -19.348 -49.581	1.00 23.67	L112 C
ATOM	1441	CD1 ILE B 128	-14.138 -16.529 -50.469	1.00 20.35	L112 C
ATOM	1442	N GLU B 129	-10.488 -19.985 -51.989	1.00 23.93	L112 N
ATOM	1443	CA GLU B 129	-9.473 -21.025 -51.982	1.00 27.79	L112 C
ATOM	1444	C GLU B 129	-8.116 -20.447 -51.612	1.00 28.96	L112 C
ATOM	1445	O GLU B 129	-7.332 -21.079 -50.907	1.00 34.08	L112 O
ATOM	1446	CB GLU B 129	-9.379 -21.666 -53.359	1.00 43.68	L112 C
ATOM	1447	CG GLU B 129	-9.007 -23.129 -53.344	1.00 54.25	L112 C
ATOM	1448	CD GLU B 129	-9.708 -23.894 -54.445	1.00 67.26	L112 C
ATOM	1449	OE1 GLU B 129	-10.697 -23.356 -54.998	1.00 58.57	L112 O
ATOM	1450	OE2 GLU B 129	-9.272 -25.027 -54.754	1.00 76.46	L112 O
ATOM	1451	N GLY B 130	-7.836 -19.248 -52.108	1.00 29.13	L112 N
ATOM	1452	CA GLY B 130	-6.571 -18.609 -51.809	1.00 23.84	L112 C
ATOM	1453	C GLY B 130	-6.440 -18.423 -50.315	1.00 27.27	L112 C
ATOM	1454	O GLY B 130	-5.372 -18.629 -49.735	1.00 29.16	L112 O
ATOM	1455	N THR B 131	-7.536 -18.031 -49.680	1.00 19.93	L112 N
ATOM	1456	CA THR B 131	-7.521 -17.839 -48.242	1.00 27.52	L112 C
ATOM	1457	C THR B 131	-7.337 -19.204 -47.579	1.00 28.05	L112 C
ATOM	1458	O THR B 131	-6.453 -19.383 -46.741	1.00 33.97	L112 O
ATOM	1459	CB THR B 131	-8.832 -17.187 -47.758	1.00 25.95	L112 C
ATOM	1460	OG1 THR B 131	-8.954 -15.883 -48.335	1.00 19.66	L112 O
ATOM	1461	CG2 THR B 131	-8.836 -17.050 -46.255	1.00 29.87	L112 C
ATOM	1462	N ALA B 132	-8.164 -20.167 -47.977	1.00 23.92	L112 N
ATOM	1463	CA ALA B 132	-8.101 -21.523 -47.436	1.00 21.36	L112 C
ATOM	1464	C ALA B 132	-6.704 -22.108 -47.505	1.00 21.61	L112 C
ATOM	1465	O ALA B 132	-6.253 -22.768 -46.575	1.00 34.50	L112 O
ATOM	1466	CB ALA B 132	-9.060 -22.428 -48.182	1.00 19.47	L112 C
ATOM	1467	N LYS B 133	-6.015 -21.870 -48.610	1.00 25.84	L112 N
ATOM	1468	CA LYS B 133	-4.674 -22.405 -48.779	1.00 29.20	L112 C
ATOM	1469	C LYS B 133	-3.693 -21.721 -47.851	1.00 27.88	L112 C
ATOM	1470	O LYS B 133	-2.642 -22.270 -47.530	1.00 37.04	L112 O
ATOM	1471	CB LYS B 133	-4.213 -22.232 -50.230	1.00 33.18	L112 C
ATOM	1472	CG LYS B 133	-5.011 -23.052 -51.235	1.00 37.46	L112 C
ATOM	1473	CD LYS B 133	-4.884 -22.487 -52.640	1.00 50.67	L112 C
ATOM	1474	CE LYS B 133	-3.636 -23.010 -53.343	1.00 51.75	L112 C
ATOM	1475	NZ LYS B 133	-3.389 -22.329 -54.654	1.00 54.53	L112 N
ATOM	1476	N SER B 134	-4.042 -20.518 -47.416	1.00 36.66	L112 N
ATOM	1477	CA SER B 134	-3.168 -19.747 -46.539	1.00 36.64	L112 C

ATOM	1478	C	SER B 134	-3.344	-20.080	-45.066	1.00	33.11	L112 C
ATOM	1479	O	SER B 134	-2.635	-19.541	-44.223	1.00	37.50	L112 O
ATOM	1480	CB	SER B 134	-3.414	-18.252	-46.741	1.00	34.18	L112 C
ATOM	1481	OG	SER B 134	-4.603	-17.857	-46.080	1.00	23.48	L112 O
ATOM	1482	N	MET B 135	-4.281	-20.964	-44.748	1.00	29.84	L112 N
ATOM	1483	CA	MET B 135	-4.509	-21.312	-43.357	1.00	23.70	L112 C
ATOM	1484	C	MET B 135	-4.602	-22.808	-43.089	1.00	29.55	L112 C
ATOM	1485	O	MET B 135	-5.283	-23.242	-42.161	1.00	23.32	L112 O
ATOM	1486	CB	MET B 135	-5.768	-20.618	-42.857	1.00	22.94	L112 C
ATOM	1487	CG	MET B 135	-7.034	-21.139	-43.448	1.00	17.81	L112 C
ATOM	1488	SD	MET B 135	-8.303	-19.898	-43.327	1.00	34.08	L112 S
ATOM	1489	CE	MET B 135	-9.264	-20.525	-41.959	1.00	35.79	L112 C
ATOM	1490	N	GLY B 136	-3.914	-23.592	-43.910	1.00	35.43	L112 N
ATOM	1491	CA	GLY B 136	-3.911	-25.030	-43.728	1.00	27.07	L112 C
ATOM	1492	C	GLY B 136	-5.245	-25.737	-43.854	1.00	28.44	L112 C
ATOM	1493	O	GLY B 136	-5.524	-26.683	-43.120	1.00	30.60	L112 O
ATOM	1494	N	ILE B 137	-6.088	-25.289	-44.770	1.00	27.95	L112 N
ATOM	1495	CA	ILE B 137	-7.357	-25.966	-44.963	1.00	31.48	L112 C
ATOM	1496	C	ILE B 137	-7.358	-26.505	-46.389	1.00	36.97	L112 C
ATOM	1497	O	ILE B 137	-7.192	-25.752	-47.350	1.00	43.45	L112 O
ATOM	1498	CB	ILE B 137	-8.547	-25.019	-44.736	1.00	31.35	L112 C
ATOM	1499	CG1	ILE B 137	-8.702	-24.756	-43.233	1.00	30.66	L112 C
ATOM	1500	CG2	ILE B 137	-9.826	-25.634	-45.302	1.00	23.26	L112 C
ATOM	1501	CD1	ILE B 137	-9.853	-23.843	-42.859	1.00	19.47	L112 C
ATOM	1502	N	GLU B 138	-7.516	-27.820	-46.508	1.00	34.70	L112 N
ATOM	1503	CA	GLU B 138	-7.523	-28.504	-47.793	1.00	24.78	L112 C
ATOM	1504	C	GLU B 138	-8.909	-28.509	-48.402	1.00	30.83	L112 C
ATOM	1505	O	GLU B 138	-9.911	-28.509	-47.685	1.00	25.06	L112 O
ATOM	1506	CB	GLU B 138	-7.065	-29.949	-47.617	1.00	33.57	L112 C
ATOM	1507	CG	GLU B 138	-5.717	-30.270	-48.240	1.00	53.60	L112 C
ATOM	1508	CD	GLU B 138	-5.435	-31.769	-48.293	1.00	61.48	L112 C
ATOM	1509	OE1	GLU B 138	-6.286	-32.555	-47.810	1.00	52.54	L112 O
ATOM	1510	OE2	GLU B 138	-4.359	-32.152	-48.818	1.00	61.92	L112 O
ATOM	1511	N	VAL B 139	-8.962	-28.518	-49.733	1.00	36.08	L112 N
ATOM	1512	CA	VAL B 139	-10.234	-28.552	-50.450	1.00	32.76	L112 C
ATOM	1513	C	VAL B 139	-10.392	-29.933	-51.077	1.00	35.50	L112 C
ATOM	1514	O	VAL B 139	-9.434	-30.484	-51.624	1.00	35.56	L112 O
ATOM	1515	CB	VAL B 139	-10.293	-27.477	-51.557	1.00	24.66	L112 C
ATOM	1516	CG1	VAL B 139	-11.653	-27.507	-52.234	1.00	22.09	L112 C
ATOM	1517	CG2	VAL B 139	-10.044	-26.102	-50.959	1.00	19.96	L112 C
ATOM	1518	N	VAL B 140	-11.593	-30.499	-50.978	1.00	39.97	L112 N
ATOM	1519	CA	VAL B 140	-11.862	-31.825	-51.534	1.00	47.65	L112 C
ATOM	1520	C	VAL B 140	-13.287	-31.934	-52.091	1.00	51.84	L112 C
ATOM	1521	O	VAL B 140	-13.610	-32.955	-52.740	1.00	48.50	L112 O
ATOM	1522	CB	VAL B 140	-11.651	-32.933	-50.467	1.00	46.88	L112 C



ATOM	1568	O1P	U C1053	14.776	-15.724	4.784	1.00	61.48	RNA1 O
ATOM	1569	O2P	U C1053	13.984	-18.106	4.231	1.00	67.30	RNA1 O
ATOM	1570	O5*	U C1053	13.059	-16.888	6.196	1.00	51.10	RNA1 O
ATOM	1571	C5*	U C1053	12.448	-18.032	6.809	1.00	47.98	RNA1 C
ATOM	1572	C4*	U C1053	11.467	-17.603	7.868	1.00	47.08	RNA1 C
ATOM	1573	O4*	U C1053	12.170	-16.895	8.917	1.00	48.31	RNA1 O
ATOM	1574	C3*	U C1053	10.382	-16.641	7.423	1.00	49.60	RNA1 C
ATOM	1575	O3*	U C1053	9.295	-17.321	6.812	1.00	61.44	RNA1 O
ATOM	1576	C2*	U C1053	9.993	-15.961	8.730	1.00	50.47	RNA1 C
ATOM	1577	O2*	U C1053	9.119	-16.731	9.531	1.00	43.66	RNA1 O
ATOM	1578	C1*	U C1053	11.339	-15.875	9.443	1.00	44.87	RNA1 C
ATOM	1579	N1	U C1053	12.003	-14.575	9.247	1.00	55.73	RNA1 N
ATOM	1580	C2	U C1053	11.564	-13.505	10.018	1.00	53.37	RNA1 C
ATOM	1581	O2	U C1053	10.644	-13.591	10.824	1.00	47.71	RNA1 O
ATOM	1582	N3	U C1053	12.240	-12.328	9.807	1.00	43.32	RNA1 N
ATOM	1583	C4	U C1053	13.281	-12.110	8.928	1.00	42.60	RNA1 C
ATOM	1584	O4	U C1053	13.827	-11.008	8.906	1.00	44.05	RNA1 O
ATOM	1585	C5	U C1053	13.666	-13.253	8.157	1.00	39.63	RNA1 C
ATOM	1586	C6	U C1053	13.032	-14.415	8.336	1.00	51.41	RNA1 C
ATOM	1587	P	G C1054	8.426	-16.576	5.682	1.00	62.77	RNA1 P
ATOM	1588	O1P	G C1054	9.391	-15.966	4.732	1.00	48.23	RNA1 O
ATOM	1589	O2P	G C1054	7.391	-17.524	5.177	1.00	63.46	RNA1 O
ATOM	1590	O5*	G C1054	7.673	-15.417	6.482	1.00	57.93	RNA1 O
ATOM	1591	C5*	G C1054	6.589	-15.737	7.376	1.00	58.01	RNA1 C
ATOM	1592	C4*	G C1054	6.160	-14.521	8.162	1.00	54.61	RNA1 C
ATOM	1593	O4*	G C1054	7.279	-14.019	8.937	1.00	57.89	RNA1 O
ATOM	1594	C3*	G C1054	5.693	-13.296	7.392	1.00	56.27	RNA1 C
ATOM	1595	O3*	G C1054	4.352	-13.378	6.946	1.00	61.66	RNA1 O
ATOM	1596	C2*	G C1054	5.851	-12.189	8.425	1.00	52.95	RNA1 C
ATOM	1597	O2*	G C1054	4.779	-12.130	9.346	1.00	49.43	RNA1 O
ATOM	1598	C1*	G C1054	7.119	-12.626	9.148	1.00	47.41	RNA1 C
ATOM	1599	N9	G C1054	8.274	-11.911	8.616	1.00	41.21	RNA1 N
ATOM	1600	C8	G C1054	9.205	-12.347	7.703	1.00	35.70	RNA1 C
ATOM	1601	N7	G C1054	10.100	-11.440	7.414	1.00	39.32	RNA1 N
ATOM	1602	C5	G C1054	9.741	-10.342	8.190	1.00	34.83	RNA1 C
ATOM	1603	C6	G C1054	10.333	-9.051	8.304	1.00	30.48	RNA1 C
ATOM	1604	O6	G C1054	11.333	-8.604	7.728	1.00	27.46	RNA1 O
ATOM	1605	N1	G C1054	9.635	-8.245	9.199	1.00	30.56	RNA1 N
ATOM	1606	C2	G C1054	8.511	-8.623	9.898	1.00	43.91	RNA1 C
ATOM	1607	N2	G C1054	7.967	-7.703	10.717	1.00	37.62	RNA1 N
ATOM	1608	N3	G C1054	7.957	-9.818	9.803	1.00	43.41	RNA1 N
ATOM	1609	C4	G C1054	8.619	-10.620	8.938	1.00	41.38	RNA1 C
ATOM	1610	P	G C1055	3.878	-12.469	5.704	1.00	66.88	RNA1 P
ATOM	1611	O1P	G C1055	4.889	-12.575	4.612	1.00	48.03	RNA1 O
ATOM	1612	O2P	G C1055	2.452	-12.820	5.440	1.00	64.70	RNA1 O

ATOM	1613	O5*	G C1055	3.943	-10.971	6.248	1.00	63.61	RNA1 O
ATOM	1614	C5*	G C1055	3.012	-10.512	7.237	1.00	53.95	RNA1 C
ATOM	1615	C4*	G C1055	3.371	-9.125	7.706	1.00	46.33	RNA1 C
ATOM	1616	O4*	G C1055	4.737	-9.107	8.201	1.00	45.69	RNA1 O
ATOM	1617	C3*	G C1055	3.363	-8.001	6.687	1.00	40.52	RNA1 C
ATOM	1618	O3*	G C1055	2.066	-7.500	6.421	1.00	47.06	RNA1 O
ATOM	1619	C2*	G C1055	4.212	-6.943	7.377	1.00	42.04	RNA1 C
ATOM	1620	O2*	G C1055	3.475	-6.224	8.348	1.00	43.70	RNA1 O
ATOM	1621	C1*	G C1055	5.264	-7.798	8.076	1.00	31.41	RNA1 C
ATOM	1622	N9	G C1055	6.501	-7.839	7.307	1.00	24.39	RNA1 N
ATOM	1623	C8	G C1055	7.026	-8.888	6.592	1.00	29.37	RNA1 C
ATOM	1624	N7	G C1055	8.158	-8.591	6.005	1.00	32.88	RNA1 N
ATOM	1625	C5	G C1055	8.388	-7.266	6.352	1.00	23.47	RNA1 C
ATOM	1626	C6	G C1055	9.458	-6.393	6.013	1.00	28.67	RNA1 C
ATOM	1627	O6	G C1055	10.450	-6.622	5.314	1.00	27.35	RNA1 O
ATOM	1628	N1	G C1055	9.292	-5.136	6.584	1.00	24.95	RNA1 N
ATOM	1629	C2	G C1055	8.235	-4.763	7.377	1.00	26.92	RNA1 C
ATOM	1630	N2	G C1055	8.255	-3.513	7.838	1.00	28.71	RNA1 N
ATOM	1631	N3	G C1055	7.234	-5.561	7.696	1.00	22.90	RNA1 N
ATOM	1632	C4	G C1055	7.375	-6.789	7.155	1.00	29.13	RNA1 C
ATOM	1633	P	G C1056	1.758	-6.834	4.989	1.00	49.25	RNA1 P
ATOM	1634	O1P	G C1056	1.991	-7.883	3.963	1.00	42.81	RNA1 O
ATOM	1635	O2P	G C1056	0.428	-6.158	5.065	1.00	37.09	RNA1 O
ATOM	1636	O5*	G C1056	2.899	-5.734	4.819	1.00	32.92	RNA1 O
ATOM	1637	C5*	G C1056	2.796	-4.457	5.476	1.00	35.07	RNA1 C
ATOM	1638	C4*	G C1056	3.939	-3.563	5.065	1.00	31.58	RNA1 C
ATOM	1639	O4*	G C1056	5.187	-4.183	5.457	1.00	35.44	RNA1 O
ATOM	1640	C3*	G C1056	4.089	-3.329	3.575	1.00	34.14	RNA1 C
ATOM	1641	O3*	G C1056	3.270	-2.275	3.113	1.00	39.89	RNA1 O
ATOM	1642	C2*	G C1056	5.567	-3.005	3.429	1.00	33.87	RNA1 C
ATOM	1643	O2*	G C1056	5.865	-1.651	3.704	1.00	36.26	RNA1 O
ATOM	1644	C1*	G C1056	6.184	-3.915	4.489	1.00	31.52	RNA1 C
ATOM	1645	N9	G C1056	6.611	-5.191	3.922	1.00	35.38	RNA1 N
ATOM	1646	C8	G C1056	5.874	-6.350	3.845	1.00	33.57	RNA1 C
ATOM	1647	N7	G C1056	6.516	-7.326	3.265	1.00	40.73	RNA1 N
ATOM	1648	C5	G C1056	7.752	-6.782	2.941	1.00	37.74	RNA1 C
ATOM	1649	C6	G C1056	8.875	-7.367	2.290	1.00	41.95	RNA1 C
ATOM	1650	O6	G C1056	8.999	-8.519	1.852	1.00	52.67	RNA1 O
ATOM	1651	N1	G C1056	9.925	-6.460	2.169	1.00	34.10	RNA1 N
ATOM	1652	C2	G C1056	9.899	-5.160	2.611	1.00	28.22	RNA1 C
ATOM	1653	N2	G C1056	11.011	-4.444	2.407	1.00	29.23	RNA1 N
ATOM	1654	N3	G C1056	8.860	-4.603	3.211	1.00	30.05	RNA1 N
ATOM	1655	C4	G C1056	7.829	-5.466	3.344	1.00	33.38	RNA1 C
ATOM	1656	P	A C1057	2.647	-2.350	1.636	1.00	36.51	RNA1 P
ATOM	1657	O1P	A C1057	2.944	-1.053	0.973	1.00	50.45	RNA1 O

ATOM	1658	O2P	A C1057	3.064	-3.614	0.988	1.00	31.54	RNA1 O
ATOM	1659	O5*	A C1057	1.085	-2.420	1.900	1.00	24.51	RNA1 O
ATOM	1660	C5*	A C1057	0.516	-3.490	2.659	1.00	23.76	RNA1 C
ATOM	1661	C4*	A C1057	-0.421	-2.936	3.703	1.00	25.17	RNA1 C
ATOM	1662	O4*	A C1057	0.346	-2.384	4.802	1.00	26.26	RNA1 O
ATOM	1663	C3*	A C1057	-1.282	-1.776	3.240	1.00	26.38	RNA1 C
ATOM	1664	O3*	A C1057	-2.429	-2.174	2.517	1.00	39.01	RNA1 O
ATOM	1665	C2*	A C1057	-1.612	-1.068	4.542	1.00	23.04	RNA1 C
ATOM	1666	O2*	A C1057	-2.658	-1.705	5.241	1.00	26.68	RNA1 O
ATOM	1667	C1*	A C1057	-0.304	-1.230	5.310	1.00	20.72	RNA1 C
ATOM	1668	N9	A C1057	0.587	-0.081	5.125	1.00	25.31	RNA1 N
ATOM	1669	C8	A C1057	1.840	-0.055	4.550	1.00	24.58	RNA1 C
ATOM	1670	N7	A C1057	2.393	1.135	4.537	1.00	16.48	RNA1 N
ATOM	1671	C5	A C1057	1.445	1.949	5.143	1.00	18.96	RNA1 C
ATOM	1672	C6	A C1057	1.428	3.322	5.438	1.00	21.91	RNA1 C
ATOM	1673	N6	A C1057	2.445	4.150	5.174	1.00	18.97	RNA1 N
ATOM	1674	N1	A C1057	0.322	3.824	6.029	1.00	28.79	RNA1 N
ATOM	1675	C2	A C1057	-0.688	2.991	6.317	1.00	26.99	RNA1 C
ATOM	1676	N3	A C1057	-0.786	1.681	6.104	1.00	27.54	RNA1 N
ATOM	1677	C4	A C1057	0.326	1.215	5.505	1.00	19.03	RNA1 C
ATOM	1678	P	U C1058	-2.943	-1.256	1.300	1.00	33.80	RNA1 P
ATOM	1679	O1P	U C1058	-1.733	-0.731	0.608	1.00	32.34	RNA1 O
ATOM	1680	O2P	U C1058	-3.967	-1.996	0.524	1.00	30.00	RNA1 O
ATOM	1681	O5*	U C1058	-3.665	-0.043	2.030	1.00	29.35	RNA1 O
ATOM	1682	C5*	U C1058	-4.955	-0.218	2.627	1.00	31.01	RNA1 C
ATOM	1683	C4*	U C1058	-5.530	1.120	3.008	1.00	33.02	RNA1 C
ATOM	1684	O4*	U C1058	-4.686	1.734	4.018	1.00	32.59	RNA1 O
ATOM	1685	C3*	U C1058	-5.554	2.156	1.902	1.00	34.36	RNA1 C
ATOM	1686	O3*	U C1058	-6.626	2.018	0.993	1.00	36.65	RNA1 O
ATOM	1687	C2*	U C1058	-5.596	3.459	2.680	1.00	27.20	RNA1 C
ATOM	1688	O2*	U C1058	-6.886	3.727	3.188	1.00	26.74	RNA1 O
ATOM	1689	C1*	U C1058	-4.652	3.139	3.831	1.00	24.15	RNA1 C
ATOM	1690	N1	U C1058	-3.267	3.546	3.532	1.00	18.02	RNA1 N
ATOM	1691	C2	U C1058	-2.971	4.898	3.590	1.00	19.91	RNA1 C
ATOM	1692	O2	U C1058	-3.802	5.750	3.879	1.00	30.16	RNA1 O
ATOM	1693	N3	U C1058	-1.671	5.219	3.300	1.00	13.57	RNA1 N
ATOM	1694	C4	U C1058	-0.655	4.353	2.965	1.00	20.26	RNA1 C
ATOM	1695	O4	U C1058	0.470	4.801	2.729	1.00	30.19	RNA1 O
ATOM	1696	C5	U C1058	-1.035	2.981	2.926	1.00	12.30	RNA1 C
ATOM	1697	C6	U C1058	-2.296	2.631	3.205	1.00	13.08	RNA1 C
ATOM	1698	P	G C1059	-6.470	2.631	-0.484	1.00	30.00	RNA1 P
ATOM	1699	O1P	G C1059	-5.071	2.397	-0.938	1.00	16.05	RNA1 O
ATOM	1700	O2P	G C1059	-7.607	2.157	-1.311	1.00	33.73	RNA1 O
ATOM	1701	O5*	G C1059	-6.635	4.196	-0.256	1.00	30.83	RNA1 O
ATOM	1702	C5*	G C1059	-7.854	4.731	0.279	1.00	22.74	RNA1 C

ATOM	1703	C4*	G C1059	-7.798	6.231	0.278	1.00	24.79	RNA1 C
ATOM	1704	O4*	G C1059	-6.727	6.667	1.149	1.00	28.49	RNA1 O
ATOM	1705	C3*	G C1059	-7.475	6.869	-1.060	1.00	26.72	RNA1 C
ATOM	1706	O3*	G C1059	-8.642	7.007	-1.857	1.00	34.13	RNA1 O
ATOM	1707	C2*	G C1059	-6.884	8.214	-0.657	1.00	28.17	RNA1 C
ATOM	1708	O2*	G C1059	-7.880	9.178	-0.371	1.00	38.10	RNA1 O
ATOM	1709	C1*	G C1059	-6.157	7.860	0.640	1.00	23.13	RNA1 C
ATOM	1710	N9	G C1059	-4.721	7.665	0.480	1.00	15.04	RNA1 N
ATOM	1711	C8	G C1059	-4.064	6.490	0.206	1.00	17.72	RNA1 C
ATOM	1712	N7	G C1059	-2.766	6.634	0.130	1.00	21.45	RNA1 N
ATOM	1713	C5	G C1059	-2.552	7.989	0.360	1.00	9.82	RNA1 C
ATOM	1714	C6	G C1059	-1.344	8.740	0.392	1.00	23.72	RNA1 C
ATOM	1715	O6	G C1059	-0.177	8.344	0.216	1.00	19.54	RNA1 O
ATOM	1716	N1	G C1059	-1.585	10.082	0.661	1.00	19.14	RNA1 N
ATOM	1717	C2	G C1059	-2.822	10.638	0.874	1.00	19.08	RNA1 C
ATOM	1718	N2	G C1059	-2.837	11.957	1.125	1.00	16.35	RNA1 N
ATOM	1719	N3	G C1059	-3.955	9.953	0.844	1.00	20.08	RNA1 N
ATOM	1720	C4	G C1059	-3.746	8.641	0.582	1.00	20.00	RNA1 C
ATOM	1721	P	U C1060	-8.509	7.045	-3.456	1.00	31.42	RNA1 P
ATOM	1722	O1P	U C1060	-9.692	6.330	-3.996	1.00	31.37	RNA1 O
ATOM	1723	O2P	U C1060	-8.243	8.446	-3.872	1.00	36.54	RNA1 O
ATOM	1724	O5*	U C1060	-7.195	6.198	-3.754	1.00	22.64	RNA1 O
ATOM	1725	C5*	U C1060	-7.016	5.523	-5.009	1.00	22.76	RNA1 C
ATOM	1726	C4*	U C1060	-5.589	5.064	-5.145	1.00	18.28	RNA1 C
ATOM	1727	O4*	U C1060	-4.739	6.232	-5.160	1.00	20.83	RNA1 O
ATOM	1728	C3*	U C1060	-5.079	4.166	-4.022	1.00	28.38	RNA1 C
ATOM	1729	O3*	U C1060	-4.142	3.234	-4.559	1.00	34.99	RNA1 O
ATOM	1730	C2*	U C1060	-4.336	5.141	-3.110	1.00	28.41	RNA1 C
ATOM	1731	O2*	U C1060	-3.277	4.523	-2.401	1.00	41.53	RNA1 O
ATOM	1732	C1*	U C1060	-3.794	6.157	-4.115	1.00	23.82	RNA1 C
ATOM	1733	N1	U C1060	-3.613	7.518	-3.587	1.00	15.63	RNA1 N
ATOM	1734	C2	U C1060	-2.336	7.922	-3.245	1.00	18.51	RNA1 C
ATOM	1735	O2	U C1060	-1.353	7.193	-3.325	1.00	21.06	RNA1 O
ATOM	1736	N3	U C1060	-2.245	9.216	-2.800	1.00	13.56	RNA1 N
ATOM	1737	C4	U C1060	-3.271	10.129	-2.661	1.00	21.90	RNA1 C
ATOM	1738	O4	U C1060	-3.015	11.281	-2.293	1.00	25.73	RNA1 O
ATOM	1739	C5	U C1060	-4.559	9.632	-3.018	1.00	7.65	RNA1 C
ATOM	1740	C6	U C1060	-4.686	8.377	-3.455	1.00	23.41	RNA1 C
ATOM	1741	P	U C1061	-4.622	2.136	-5.633	1.00	28.90	RNA1 P
ATOM	1742	O1P	U C1061	-3.994	0.840	-5.253	1.00	34.87	RNA1 O
ATOM	1743	O2P	U C1061	-6.093	2.222	-5.792	1.00	16.57	RNA1 O
ATOM	1744	O5*	U C1061	-3.946	2.631	-6.983	1.00	24.02	RNA1 O
ATOM	1745	C5*	U C1061	-2.514	2.667	-7.117	1.00	25.58	RNA1 C
ATOM	1746	C4*	U C1061	-2.122	3.503	-8.311	1.00	31.26	RNA1 C
ATOM	1747	O4*	U C1061	-2.694	2.914	-9.507	1.00	36.66	RNA1 O



ATOM	1748	C3*	U C1061	-2.584	4.961	-8.290	1.00	33.14	RNA1 C
ATOM	1749	O3*	U C1061	-1.601	5.740	-8.967	1.00	23.50	RNA1 O
ATOM	1750	C2*	U C1061	-3.831	4.934	-9.167	1.00	32.29	RNA1 C
ATOM	1751	O2*	U C1061	-4.100	6.183	-9.775	1.00	33.30	RNA1 O
ATOM	1752	C1*	U C1061	-3.414	3.896	-10.205	1.00	40.61	RNA1 C
ATOM	1753	N1	U C1061	-4.461	3.257	-11.015	1.00	50.51	RNA1 N
ATOM	1754	C2	U C1061	-4.299	3.335	-12.387	1.00	62.28	RNA1 C
ATOM	1755	O2	U C1061	-3.330	3.880	-12.914	1.00	62.30	RNA1 O
ATOM	1756	N3	U C1061	-5.303	2.754	-13.123	1.00	73.69	RNA1 N
ATOM	1757	C4	U C1061	-6.427	2.110	-12.641	1.00	67.10	RNA1 C
ATOM	1758	O4	U C1061	-7.260	1.668	-13.440	1.00	68.66	RNA1 O
ATOM	1759	C5	U C1061	-6.515	2.056	-11.210	1.00	54.52	RNA1 C
ATOM	1760	C6	U C1061	-5.552	2.617	-10.463	1.00	45.73	RNA1 C
ATOM	1761	P	G C1062	-0.570	6.637	-8.138	1.00	27.54	RNA1 P
ATOM	1762	O1P	G C1062	-0.356	5.986	-6.813	1.00	24.54	RNA1 O
ATOM	1763	O2P	G C1062	0.600	6.908	-9.017	1.00	15.00	RNA1 O
ATOM	1764	O5*	G C1062	-1.358	8.001	-7.930	1.00	14.13	RNA1 O
ATOM	1765	C5*	G C1062	-2.396	8.125	-6.939	1.00	22.88	RNA1 C
ATOM	1766	C4*	G C1062	-2.448	9.547	-6.435	1.00	15.45	RNA1 C
ATOM	1767	O4*	G C1062	-1.246	9.824	-5.677	1.00	24.75	RNA1 O
ATOM	1768	C3*	G C1062	-2.438	10.568	-7.550	1.00	12.59	RNA1 C
ATOM	1769	O3*	G C1062	-3.742	10.823	-8.006	1.00	33.25	RNA1 O
ATOM	1770	C2*	G C1062	-1.783	11.777	-6.911	1.00	19.71	RNA1 C
ATOM	1771	O2*	G C1062	-2.709	12.520	-6.141	1.00	23.78	RNA1 O
ATOM	1772	C1*	G C1062	-0.751	11.111	-5.999	1.00	16.39	RNA1 C
ATOM	1773	N9	G C1062	0.564	10.927	-6.611	1.00	14.13	RNA1 N
ATOM	1774	C8	G C1062	1.229	9.734	-6.776	1.00	24.14	RNA1 C
ATOM	1775	N7	G C1062	2.388	9.866	-7.361	1.00	25.47	RNA1 N
ATOM	1776	C5	G C1062	2.495	11.229	-7.605	1.00	26.26	RNA1 C
ATOM	1777	C6	G C1062	3.527	11.966	-8.235	1.00	31.66	RNA1 C
ATOM	1778	O6	G C1062	4.572	11.542	-8.758	1.00	28.31	RNA1 O
ATOM	1779	N1	G C1062	3.246	13.328	-8.243	1.00	23.22	RNA1 N
ATOM	1780	C2	G C1062	2.108	13.904	-7.739	1.00	23.93	RNA1 C
ATOM	1781	N2	G C1062	2.025	15.238	-7.844	1.00	18.71	RNA1 N
ATOM	1782	N3	G C1062	1.125	13.226	-7.174	1.00	19.22	RNA1 N
ATOM	1783	C4	G C1062	1.384	11.902	-7.137	1.00	21.18	RNA1 C
ATOM	1784	P	G C1063	-3.983	11.091	-9.564	1.00	32.90	RNA1 P
ATOM	1785	O1P	G C1063	-3.162	10.105	-10.324	1.00	29.07	RNA1 O
ATOM	1786	O2P	G C1063	-5.446	11.159	-9.776	1.00	28.95	RNA1 O
ATOM	1787	O5*	G C1063	-3.361	12.534	-9.798	1.00	32.11	RNA1 O
ATOM	1788	C5*	G C1063	-4.042	13.712	-9.342	1.00	23.86	RNA1 C
ATOM	1789	C4*	G C1063	-3.302	14.944	-9.798	1.00	22.38	RNA1 C
ATOM	1790	O4*	G C1063	-1.983	14.950	-9.201	1.00	24.88	RNA1 O
ATOM	1791	C3*	G C1063	-3.019	15.022	-11.287	1.00	26.89	RNA1 C
ATOM	1792	O3*	G C1063	-4.110	15.506	-12.042	1.00	33.17	RNA1 O

ATOM	1793	C2*	G C1063	-1.806	15.936	-11.343	1.00	25.82	RNA1 C
ATOM	1794	O2*	G C1063	-2.149	17.294	-11.168	1.00	34.75	RNA1 O
ATOM	1795	C1*	G C1063	-1.035	15.472	-10.118	1.00	14.96	RNA1 C
ATOM	1796	N9	G C1063	-0.093	14.412	-10.461	1.00	16.28	RNA1 N
ATOM	1797	C8	G C1063	-0.201	13.070	-10.178	1.00	17.00	RNA1 C
ATOM	1798	N7	G C1063	0.820	12.373	-10.602	1.00	23.95	RNA1 N
ATOM	1799	C5	G C1063	1.644	13.309	-11.212	1.00	13.66	RNA1 C
ATOM	1800	C6	G C1063	2.898	13.151	-11.857	1.00	19.46	RNA1 C
ATOM	1801	O6	G C1063	3.555	12.117	-12.032	1.00	27.29	RNA1 O
ATOM	1802	N1	G C1063	3.385	14.363	-12.326	1.00	19.82	RNA1 N
ATOM	1803	C2	G C1063	2.749	15.571	-12.201	1.00	24.09	RNA1 C
ATOM	1804	N2	G C1063	3.385	16.631	-12.718	1.00	33.27	RNA1 N
ATOM	1805	N3	G C1063	1.579	15.731	-11.609	1.00	25.48	RNA1 N
ATOM	1806	C4	G C1063	1.091	14.569	-11.137	1.00	16.05	RNA1 C
ATOM	1807	P	C C1064	-4.385	14.882	-13.495	1.00	32.63	RNA1 P
ATOM	1808	O1P	C C1064	-4.311	13.399	-13.376	1.00	34.14	RNA1 O
ATOM	1809	O2P	C C1064	-5.610	15.520	-14.047	1.00	34.53	RNA1 O
ATOM	1810	O5*	C C1064	-3.124	15.351	-14.340	1.00	25.39	RNA1 O
ATOM	1811	C5*	C C1064	-2.841	16.743	-14.483	1.00	20.47	RNA1 C
ATOM	1812	C4*	C C1064	-1.510	16.945	-15.158	1.00	22.15	RNA1 C
ATOM	1813	O4*	C C1064	-0.455	16.348	-14.362	1.00	25.83	RNA1 O
ATOM	1814	C3*	C C1064	-1.320	16.321	-16.528	1.00	29.48	RNA1 C
ATOM	1815	O3*	C C1064	-1.921	17.088	-17.565	1.00	35.84	RNA1 O
ATOM	1816	C2*	C C1064	0.199	16.267	-16.648	1.00	29.04	RNA1 C
ATOM	1817	O2*	C C1064	0.774	17.500	-17.036	1.00	28.73	RNA1 O
ATOM	1818	C1*	C C1064	0.611	15.958	-15.212	1.00	21.28	RNA1 C
ATOM	1819	N1	C C1064	0.899	14.525	-15.020	1.00	19.09	RNA1 N
ATOM	1820	C2	C C1064	2.155	14.044	-15.409	1.00	27.83	RNA1 C
ATOM	1821	O2	C C1064	2.977	14.836	-15.897	1.00	32.73	RNA1 O
ATOM	1822	N3	C C1064	2.442	12.734	-15.247	1.00	23.67	RNA1 N
ATOM	1823	C4	C C1064	1.535	11.915	-14.716	1.00	22.40	RNA1 C
ATOM	1824	N4	C C1064	1.871	10.635	-14.564	1.00	29.03	RNA1 N
ATOM	1825	C5	C C1064	0.246	12.374	-14.314	1.00	9.70	RNA1 C
ATOM	1826	C6	C C1064	-0.027	13.674	-14.482	1.00	20.34	RNA1 C
ATOM	1827	P	U C1065	-2.537	16.339	-18.853	1.00	31.56	RNA1 P
ATOM	1828	O1P	U C1065	-3.488	15.293	-18.407	1.00	29.35	RNA1 O
ATOM	1829	O2P	U C1065	-3.011	17.398	-19.774	1.00	46.70	RNA1 O
ATOM	1830	O5*	U C1065	-1.266	15.617	-19.495	1.00	22.04	RNA1 O
ATOM	1831	C5*	U C1065	-0.138	16.392	-19.935	1.00	25.90	RNA1 C
ATOM	1832	C4*	U C1065	1.022	15.492	-20.286	1.00	32.86	RNA1 C
ATOM	1833	O4*	U C1065	1.493	14.818	-19.094	1.00	35.71	RNA1 O
ATOM	1834	C3*	U C1065	0.721	14.374	-21.270	1.00	35.55	RNA1 C
ATOM	1835	O3*	U C1065	0.799	14.834	-22.609	1.00	37.39	RNA1 O
ATOM	1836	C2*	U C1065	1.793	13.340	-20.939	1.00	36.11	RNA1 C
ATOM	1837	O2*	U C1065	3.047	13.612	-21.536	1.00	27.98	RNA1 O

ATOM	1838	C1*	U C1065	1.917	13.505	-19.423	1.00	33.40	RNA1 C
ATOM	1839	N1	U C1065	1.088	12.543	-18.676	1.00	17.15	RNA1 N
ATOM	1840	C2	U C1065	1.653	11.323	-18.364	1.00	21.75	RNA1 C
ATOM	1841	O2	U C1065	2.789	11.015	-18.700	1.00	24.53	RNA1 O
ATOM	1842	N3	U C1065	0.841	10.472	-17.652	1.00	12.86	RNA1 N
ATOM	1843	C4	U C1065	-0.454	10.708	-17.245	1.00	22.54	RNA1 C
ATOM	1844	O4	U C1065	-1.068	9.829	-16.631	1.00	33.30	RNA1 O
ATOM	1845	C5	U C1065	-0.972	11.988	-17.617	1.00	18.28	RNA1 C
ATOM	1846	C6	U C1065	-0.202	12.840	-18.300	1.00	12.72	RNA1 C
ATOM	1847	P	U C1066	-0.290	14.345	-23.688	1.00	38.85	RNA1 P
ATOM	1848	O1P	U C1066	-1.664	14.499	-23.126	1.00	18.29	RNA1 O
ATOM	1849	O2P	U C1066	0.064	15.034	-24.964	1.00	40.95	RNA1 O
ATOM	1850	O5*	U C1066	0.014	12.790	-23.851	1.00	36.40	RNA1 O
ATOM	1851	C5*	U C1066	1.288	12.346	-24.350	1.00	35.84	RNA1 C
ATOM	1852	C4*	U C1066	1.461	10.870	-24.107	1.00	38.35	RNA1 C
ATOM	1853	O4*	U C1066	1.463	10.613	-22.679	1.00	39.66	RNA1 O
ATOM	1854	C3*	U C1066	0.359	9.974	-24.652	1.00	44.84	RNA1 C
ATOM	1855	O3*	U C1066	0.570	9.660	-26.021	1.00	45.33	RNA1 O
ATOM	1856	C2*	U C1066	0.473	8.739	-23.769	1.00	44.55	RNA1 C
ATOM	1857	O2*	U C1066	1.511	7.884	-24.213	1.00	33.40	RNA1 O
ATOM	1858	C1*	U C1066	0.859	9.357	-22.421	1.00	39.47	RNA1 C
ATOM	1859	N1	U C1066	-0.301	9.556	-21.535	1.00	27.32	RNA1 N
ATOM	1860	C2	U C1066	-0.598	8.548	-20.630	1.00	27.94	RNA1 C
ATOM	1861	O2	U C1066	0.086	7.545	-20.506	1.00	31.42	RNA1 O
ATOM	1862	N3	U C1066	-1.722	8.759	-19.869	1.00	19.18	RNA1 N
ATOM	1863	C4	U C1066	-2.556	9.854	-19.905	1.00	25.49	RNA1 C
ATOM	1864	O4	U C1066	-3.565	9.870	-19.194	1.00	36.42	RNA1 O
ATOM	1865	C5	U C1066	-2.168	10.867	-20.840	1.00	19.93	RNA1 C
ATOM	1866	C6	U C1066	-1.082	10.689	-21.604	1.00	23.45	RNA1 C
ATOM	1867	P	A C1067	-0.690	9.514	-27.002	1.00	46.85	RNA1 P
ATOM	1868	O1P	A C1067	-1.666	10.598	-26.712	1.00	36.17	RNA1 O
ATOM	1869	O2P	A C1067	-0.149	9.350	-28.374	1.00	52.36	RNA1 O
ATOM	1870	O5*	A C1067	-1.379	8.151	-26.562	1.00	45.01	RNA1 O
ATOM	1871	C5*	A C1067	-2.763	7.888	-26.874	1.00	42.12	RNA1 C
ATOM	1872	C4*	A C1067	-3.108	6.464	-26.511	1.00	37.93	RNA1 C
ATOM	1873	O4*	A C1067	-2.272	5.567	-27.279	1.00	37.30	RNA1 O
ATOM	1874	C3*	A C1067	-2.805	6.123	-25.068	1.00	39.89	RNA1 C
ATOM	1875	O3*	A C1067	-3.905	6.462	-24.244	1.00	44.47	RNA1 O
ATOM	1876	C2*	A C1067	-2.505	4.632	-25.107	1.00	27.28	RNA1 C
ATOM	1877	O2*	A C1067	-3.664	3.829	-25.084	1.00	44.22	RNA1 O
ATOM	1878	C1*	A C1067	-1.845	4.494	-26.472	1.00	20.11	RNA1 C
ATOM	1879	N9	A C1067	-0.389	4.519	-26.443	1.00	16.55	RNA1 N
ATOM	1880	C8	A C1067	0.450	5.516	-26.872	1.00	13.35	RNA1 C
ATOM	1881	N7	A C1067	1.722	5.206	-26.785	1.00	21.36	RNA1 N
ATOM	1882	C5	A C1067	1.715	3.927	-26.244	1.00	6.97	RNA1 C

TOTAL: 5035000

ATOM	1883	C6	A C1067	2.746	3.037	-25.917	1.00	18.48	RNA1 C
ATOM	1884	N6	A C1067	4.046	3.301	-26.105	1.00	25.96	RNA1 N
ATOM	1885	N1	A C1067	2.400	1.845	-25.391	1.00	13.59	RNA1 N
ATOM	1886	C2	A C1067	1.102	1.575	-25.214	1.00	28.55	RNA1 C
ATOM	1887	N3	A C1067	0.041	2.326	-25.488	1.00	23.97	RNA1 N
ATOM	1888	C4	A C1067	0.423	3.503	-26.009	1.00	16.34	RNA1 C
ATOM	1889	P	G C1068	-3.632	7.060	-22.783	1.00	39.02	RNA1 P
ATOM	1890	O1P	G C1068	-2.666	8.189	-22.930	1.00	31.97	RNA1 O
ATOM	1891	O2P	G C1068	-4.955	7.282	-22.122	1.00	23.85	RNA1 O
ATOM	1892	O5*	G C1068	-2.872	5.872	-22.052	1.00	29.64	RNA1 O
ATOM	1893	C5*	G C1068	-3.560	4.650	-21.753	1.00	26.14	RNA1 C
ATOM	1894	C4*	G C1068	-2.611	3.675	-21.128	1.00	30.68	RNA1 C
ATOM	1895	O4*	G C1068	-1.612	3.299	-22.105	1.00	33.92	RNA1 O
ATOM	1896	C3*	G C1068	-1.821	4.231	-19.956	1.00	37.79	RNA1 C
ATOM	1897	O3*	G C1068	-2.586	4.140	-18.752	1.00	40.54	RNA1 O
ATOM	1898	C2*	G C1068	-0.564	3.368	-19.963	1.00	31.49	RNA1 C
ATOM	1899	O2*	G C1068	-0.774	2.123	-19.322	1.00	38.55	RNA1 O
ATOM	1900	C1*	G C1068	-0.364	3.120	-21.463	1.00	28.77	RNA1 C
ATOM	1901	N9	G C1068	0.605	3.989	-22.123	1.00	18.63	RNA1 N
ATOM	1902	C8	G C1068	0.381	5.255	-22.612	1.00	21.10	RNA1 C
ATOM	1903	N7	G C1068	1.437	5.779	-23.177	1.00	18.47	RNA1 N
ATOM	1904	C5	G C1068	2.419	4.808	-23.047	1.00	12.57	RNA1 C
ATOM	1905	C6	G C1068	3.776	4.807	-23.476	1.00	23.53	RNA1 C
ATOM	1906	O6	G C1068	4.402	5.696	-24.076	1.00	26.90	RNA1 O
ATOM	1907	N1	G C1068	4.417	3.616	-23.140	1.00	26.41	RNA1 N
ATOM	1908	C2	G C1068	3.831	2.561	-22.479	1.00	23.88	RNA1 C
ATOM	1909	N2	G C1068	4.625	1.500	-22.232	1.00	22.10	RNA1 N
ATOM	1910	N3	G C1068	2.564	2.546	-22.085	1.00	17.30	RNA1 N
ATOM	1911	C4	G C1068	1.924	3.695	-22.396	1.00	15.61	RNA1 C
ATOM	1912	P	A C1069	-2.674	5.408	-17.758	1.00	35.85	RNA1 P
ATOM	1913	O1P	A C1069	-2.982	6.639	-18.536	1.00	34.22	RNA1 O
ATOM	1914	O2P	A C1069	-3.551	5.029	-16.625	1.00	34.69	RNA1 O
ATOM	1915	O5*	A C1069	-1.186	5.532	-17.220	1.00	22.83	RNA1 O
ATOM	1916	C5*	A C1069	-0.570	4.437	-16.545	1.00	16.26	RNA1 C
ATOM	1917	C4*	A C1069	0.859	4.768	-16.237	1.00	21.94	RNA1 C
ATOM	1918	O4*	A C1069	1.694	4.585	-17.417	1.00	35.64	RNA1 O
ATOM	1919	C3*	A C1069	1.093	6.209	-15.768	1.00	37.69	RNA1 C
ATOM	1920	O3*	A C1069	2.058	6.196	-14.714	1.00	40.68	RNA1 O
ATOM	1921	C2*	A C1069	1.737	6.855	-16.996	1.00	39.67	RNA1 C
ATOM	1922	O2*	A C1069	2.583	7.960	-16.731	1.00	43.60	RNA1 O
ATOM	1923	C1*	A C1069	2.567	5.680	-17.491	1.00	37.65	RNA1 C
ATOM	1924	N9	A C1069	3.223	5.772	-18.793	1.00	33.82	RNA1 N
ATOM	1925	C8	A C1069	2.972	6.600	-19.858	1.00	28.66	RNA1 C
ATOM	1926	N7	A C1069	3.878	6.527	-20.805	1.00	37.91	RNA1 N
ATOM	1927	C5	A C1069	4.758	5.554	-20.349	1.00	34.14	RNA1 C

ATOM	1928	C6	A C1069	5.949	5.022	-20.886	1.00	38.86	RNA1 C
ATOM	1929	N6	A C1069	6.490	5.420	-22.038	1.00	44.62	RNA1 N
ATOM	1930	N1	A C1069	6.577	4.054	-20.180	1.00	40.40	RNA1 N
ATOM	1931	C2	A C1069	6.041	3.661	-19.017	1.00	35.55	RNA1 C
ATOM	1932	N3	A C1069	4.939	4.093	-18.408	1.00	28.51	RNA1 N
ATOM	1933	C4	A C1069	4.342	5.053	-19.133	1.00	31.82	RNA1 C
ATOM	1934	P	A C1070	1.715	6.875	-13.302	1.00	33.11	RNA1 P
ATOM	1935	O1P	A C1070	3.039	7.134	-12.680	1.00	18.08	RNA1 O
ATOM	1936	O2P	A C1070	0.734	7.989	-13.469	1.00	18.52	RNA1 O
ATOM	1937	O5*	A C1070	0.968	5.723	-12.497	1.00	30.46	RNA1 O
ATOM	1938	C5*	A C1070	1.690	4.589	-11.998	1.00	21.05	RNA1 C
ATOM	1939	C4*	A C1070	0.844	3.851	-11.000	1.00	30.01	RNA1 C
ATOM	1940	O4*	A C1070	-0.391	3.424	-11.634	1.00	25.30	RNA1 O
ATOM	1941	C3*	A C1070	1.479	2.612	-10.390	1.00	36.56	RNA1 C
ATOM	1942	O3*	A C1070	1.078	2.564	-9.026	1.00	37.18	RNA1 O
ATOM	1943	C2*	A C1070	0.847	1.469	-11.185	1.00	37.06	RNA1 C
ATOM	1944	O2*	A C1070	0.739	0.256	-10.463	1.00	48.87	RNA1 O
ATOM	1945	C1*	A C1070	-0.539	2.028	-11.495	1.00	32.98	RNA1 C
ATOM	1946	N9	A C1070	-1.107	1.501	-12.735	1.00	42.72	RNA1 N
ATOM	1947	C8	A C1070	-0.659	1.702	-14.019	1.00	49.93	RNA1 C
ATOM	1948	N7	A C1070	-1.380	1.098	-14.929	1.00	50.90	RNA1 N
ATOM	1949	C5	A C1070	-2.366	0.452	-14.198	1.00	55.33	RNA1 C
ATOM	1950	C6	A C1070	-3.435	-0.367	-14.582	1.00	59.78	RNA1 C
ATOM	1951	N6	A C1070	-3.697	-0.683	-15.850	1.00	68.95	RNA1 N
ATOM	1952	N1	A C1070	-4.235	-0.857	-13.608	1.00	56.29	RNA1 N
ATOM	1953	C2	A C1070	-3.965	-0.536	-12.340	1.00	41.79	RNA1 C
ATOM	1954	N3	A C1070	-2.987	0.222	-11.854	1.00	44.24	RNA1 N
ATOM	1955	C4	A C1070	-2.212	0.692	-12.847	1.00	46.56	RNA1 C
ATOM	1956	P	G C1071	2.022	1.866	-7.940	1.00	29.75	RNA1 P
ATOM	1957	O1P	G C1071	1.299	1.985	-6.653	1.00	39.09	RNA1 O
ATOM	1958	O2P	G C1071	2.436	0.526	-8.435	1.00	39.01	RNA1 O
ATOM	1959	O5*	G C1071	3.325	2.769	-7.901	1.00	19.92	RNA1 O
ATOM	1960	C5*	G C1071	3.295	4.113	-7.406	1.00	16.74	RNA1 C
ATOM	1961	C4*	G C1071	4.704	4.562	-7.133	1.00	23.89	RNA1 C
ATOM	1962	O4*	G C1071	5.222	3.769	-6.044	1.00	22.65	RNA1 O
ATOM	1963	C3*	G C1071	5.633	4.285	-8.302	1.00	25.19	RNA1 C
ATOM	1964	O3*	G C1071	5.646	5.390	-9.187	1.00	38.67	RNA1 O
ATOM	1965	C2*	G C1071	6.974	4.006	-7.639	1.00	21.49	RNA1 C
ATOM	1966	O2*	G C1071	7.729	5.164	-7.347	1.00	30.27	RNA1 O
ATOM	1967	C1*	G C1071	6.533	3.335	-6.340	1.00	18.58	RNA1 C
ATOM	1968	N9	G C1071	6.500	1.878	-6.393	1.00	22.64	RNA1 N
ATOM	1969	C8	G C1071	5.389	1.076	-6.272	1.00	20.39	RNA1 C
ATOM	1970	N7	G C1071	5.672	-0.196	-6.315	1.00	31.29	RNA1 N
ATOM	1971	C5	G C1071	7.048	-0.236	-6.482	1.00	14.55	RNA1 C
ATOM	1972	C6	G C1071	7.922	-1.342	-6.582	1.00	28.22	RNA1 C

ATOM	1973	O6	G C1071	7.647	-2.549	-6.512	1.00	31.85	RNA1 O
ATOM	1974	N1	G C1071	9.239	-0.934	-6.762	1.00	15.53	RNA1 N
ATOM	1975	C2	G C1071	9.660	0.371	-6.818	1.00	20.27	RNA1 C
ATOM	1976	N2	G C1071	10.977	0.567	-6.997	1.00	25.10	RNA1 N
ATOM	1977	N3	G C1071	8.853	1.411	-6.707	1.00	19.36	RNA1 N
ATOM	1978	C4	G C1071	7.570	1.035	-6.546	1.00	11.18	RNA1 C
ATOM	1979	P	C C1072	5.597	5.137	-10.767	1.00	27.21	RNA1 P
ATOM	1980	O1P	C C1072	4.563	4.110	-11.043	1.00	30.50	RNA1 O
ATOM	1981	O2P	C C1072	5.512	6.459	-11.426	1.00	25.77	RNA1 O
ATOM	1982	O5*	C C1072	7.022	4.506	-11.073	1.00	15.96	RNA1 O
ATOM	1983	C5*	C C1072	8.198	5.315	-11.019	1.00	23.11	RNA1 C
ATOM	1984	C4*	C C1072	9.419	4.471	-11.280	1.00	32.01	RNA1 C
ATOM	1985	O4*	C C1072	9.601	3.533	-10.192	1.00	36.03	RNA1 O
ATOM	1986	C3*	C C1072	9.365	3.597	-12.522	1.00	30.99	RNA1 C
ATOM	1987	O3*	C C1072	9.711	4.326	-13.688	1.00	33.23	RNA1 O
ATOM	1988	C2*	C C1072	10.362	2.496	-12.188	1.00	29.75	RNA1 C
ATOM	1989	O2*	C C1072	11.703	2.904	-12.371	1.00	34.64	RNA1 O
ATOM	1990	C1*	C C1072	10.121	2.314	-10.692	1.00	29.06	RNA1 C
ATOM	1991	N1	C C1072	9.151	1.242	-10.401	1.00	21.88	RNA1 N
ATOM	1992	C2	C C1072	9.623	-0.062	-10.229	1.00	22.42	RNA1 C
ATOM	1993	O2	C C1072	10.852	-0.281	-10.328	1.00	27.87	RNA1 O
ATOM	1994	N3	C C1072	8.735	-1.053	-9.964	1.00	9.91	RNA1 N
ATOM	1995	C4	C C1072	7.430	-0.780	-9.883	1.00	19.29	RNA1 C
ATOM	1996	N4	C C1072	6.591	-1.789	-9.644	1.00	23.91	RNA1 N
ATOM	1997	C5	C C1072	6.925	0.538	-10.048	1.00	13.70	RNA1 C
ATOM	1998	C6	C C1072	7.812	1.510	-10.304	1.00	24.95	RNA1 C
ATOM	1999	P	A C1073	8.702	4.336	-14.936	1.00	33.99	RNA1 P
ATOM	2000	O1P	A C1073	8.504	2.919	-15.333	1.00	35.83	RNA1 O
ATOM	2001	O2P	A C1073	7.512	5.181	-14.614	1.00	22.96	RNA1 O
ATOM	2002	O5*	A C1073	9.551	5.050	-16.074	1.00	31.36	RNA1 O
ATOM	2003	C5*	A C1073	10.772	4.462	-16.571	1.00	35.37	RNA1 C
ATOM	2004	C4*	A C1073	11.245	5.227	-17.781	1.00	39.45	RNA1 C
ATOM	2005	O4*	A C1073	10.229	5.143	-18.815	1.00	39.78	RNA1 O
ATOM	2006	C3*	A C1073	11.400	6.713	-17.522	1.00	40.87	RNA1 C
ATOM	2007	O3*	A C1073	12.673	7.017	-16.987	1.00	44.46	RNA1 O
ATOM	2008	C2*	A C1073	11.147	7.327	-18.890	1.00	38.57	RNA1 C
ATOM	2009	O2*	A C1073	12.279	7.252	-19.738	1.00	41.89	RNA1 O
ATOM	2010	C1*	A C1073	10.054	6.409	-19.426	1.00	27.18	RNA1 C
ATOM	2011	N9	A C1073	8.713	6.872	-19.081	1.00	23.78	RNA1 N
ATOM	2012	C8	A C1073	7.835	6.282	-18.209	1.00	31.10	RNA1 C
ATOM	2013	N7	A C1073	6.685	6.903	-18.112	1.00	30.54	RNA1 N
ATOM	2014	C5	A C1073	6.819	7.979	-18.974	1.00	22.89	RNA1 C
ATOM	2015	C6	A C1073	5.948	9.015	-19.319	1.00	24.05	RNA1 C
ATOM	2016	N6	A C1073	4.711	9.130	-18.836	1.00	24.67	RNA1 N
ATOM	2017	N1	A C1073	6.391	9.940	-20.193	1.00	27.06	RNA1 N

ATOM	2018	C2	A C1073	7.627	9.815	-20.684	1.00	28.92	RNA1 C
ATOM	2019	N3	A C1073	8.539	8.879	-20.442	1.00	33.22	RNA1 N
ATOM	2020	C4	A C1073	8.066	7.979	-19.568	1.00	24.70	RNA1 C
ATOM	2021	P	G C1074	12.790	8.131	-15.846	1.00	37.49	RNA1 P
ATOM	2022	O1P	G C1074	11.994	7.638	-14.698	1.00	42.76	RNA1 O
ATOM	2023	O2P	G C1074	14.226	8.458	-15.661	1.00	37.27	RNA1 O
ATOM	2024	O5*	G C1074	12.052	9.389	-16.488	1.00	32.12	RNA1 O
ATOM	2025	C5*	G C1074	12.636	10.074	-17.611	1.00	30.38	RNA1 C
ATOM	2026	C4*	G C1074	11.776	11.239	-18.042	1.00	29.26	RNA1 C
ATOM	2027	O4*	G C1074	10.505	10.762	-18.552	1.00	28.39	RNA1 O
ATOM	2028	C3*	G C1074	11.393	12.245	-16.972	1.00	30.49	RNA1 C
ATOM	2029	O3*	G C1074	12.431	13.170	-16.697	1.00	40.29	RNA1 O
ATOM	2030	C2*	G C1074	10.152	12.899	-17.566	1.00	32.10	RNA1 C
ATOM	2031	O2*	G C1074	10.452	13.891	-18.528	1.00	36.08	RNA1 O
ATOM	2032	C1*	G C1074	9.491	11.714	-18.268	1.00	26.45	RNA1 C
ATOM	2033	N9	G C1074	8.479	11.075	-17.435	1.00	22.10	RNA1 N
ATOM	2034	C8	G C1074	8.576	9.862	-16.794	1.00	21.18	RNA1 C
ATOM	2035	N7	G C1074	7.490	9.539	-16.145	1.00	28.77	RNA1 N
ATOM	2036	C5	G C1074	6.628	10.604	-16.362	1.00	15.54	RNA1 C
ATOM	2037	C6	G C1074	5.300	10.815	-15.917	1.00	22.89	RNA1 C
ATOM	2038	O6	G C1074	4.589	10.071	-15.240	1.00	28.81	RNA1 O
ATOM	2039	N1	G C1074	4.802	12.038	-16.351	1.00	26.73	RNA1 N
ATOM	2040	C2	G C1074	5.487	12.937	-17.126	1.00	24.75	RNA1 C
ATOM	2041	N2	G C1074	4.828	14.058	-17.440	1.00	20.91	RNA1 N
ATOM	2042	N3	G C1074	6.724	12.748	-17.560	1.00	19.40	RNA1 N
ATOM	2043	C4	G C1074	7.228	11.568	-17.144	1.00	19.49	RNA1 C
ATOM	2044	P	C C1075	12.535	13.826	-15.232	1.00	35.74	RNA1 P
ATOM	2045	O1P	C C1075	12.251	12.757	-14.239	1.00	37.48	RNA1 O
ATOM	2046	O2P	C C1075	13.814	14.574	-15.147	1.00	35.45	RNA1 O
ATOM	2047	O5*	C C1075	11.326	14.864	-15.223	1.00	29.10	RNA1 O
ATOM	2048	C5*	C C1075	11.373	16.035	-16.052	1.00	20.72	RNA1 C
ATOM	2049	C4*	C C1075	10.144	16.884	-15.848	1.00	27.73	RNA1 C
ATOM	2050	O4*	C C1075	8.980	16.162	-16.316	1.00	25.49	RNA1 O
ATOM	2051	C3*	C C1075	9.804	17.254	-14.413	1.00	29.84	RNA1 C
ATOM	2052	O3*	C C1075	10.548	18.355	-13.924	1.00	32.76	RNA1 O
ATOM	2053	C2*	C C1075	8.311	17.537	-14.490	1.00	32.29	RNA1 C
ATOM	2054	O2*	C C1075	8.018	18.838	-14.963	1.00	33.04	RNA1 O
ATOM	2055	C1*	C C1075	7.860	16.488	-15.508	1.00	30.74	RNA1 C
ATOM	2056	N1	C C1075	7.407	15.259	-14.836	1.00	23.00	RNA1 N
ATOM	2057	C2	C C1075	6.083	15.178	-14.407	1.00	25.39	RNA1 C
ATOM	2058	O2	C C1075	5.320	16.133	-14.627	1.00	27.71	RNA1 O
ATOM	2059	N3	C C1075	5.666	14.063	-13.764	1.00	20.56	RNA1 N
ATOM	2060	C4	C C1075	6.518	13.054	-13.553	1.00	24.69	RNA1 C
ATOM	2061	N4	C C1075	6.067	11.975	-12.911	1.00	22.56	RNA1 N
ATOM	2062	C5	C C1075	7.870	13.108	-13.991	1.00	16.20	RNA1 C

ATOM	2063	C6	C C1075	8.269	14.217	-14.622	1.00	23.77	RNA1 C
ATOM	2064	P	C C1076	10.912	18.423	-12.358	1.00	42.91	RNA1 P
ATOM	2065	O1P	C C1076	11.372	17.085	-11.911	1.00	24.52	RNA1 O
ATOM	2066	O2P	C C1076	11.781	19.612	-12.113	1.00	41.73	RNA1 O
ATOM	2067	O5*	C C1076	9.491	18.679	-11.696	1.00	32.86	RNA1 O
ATOM	2068	C5*	C C1076	8.768	19.870	-11.997	1.00	27.46	RNA1 C
ATOM	2069	C4*	C C1076	7.458	19.893	-11.255	1.00	30.86	RNA1 C
ATOM	2070	O4*	C C1076	6.570	18.885	-11.798	1.00	34.77	RNA1 O
ATOM	2071	C3*	C C1076	7.500	19.581	-9.769	1.00	26.66	RNA1 C
ATOM	2072	O3*	C C1076	7.913	20.668	-8.961	1.00	36.57	RNA1 O
ATOM	2073	C2*	C C1076	6.062	19.172	-9.499	1.00	32.47	RNA1 C
ATOM	2074	O2*	C C1076	5.198	20.290	-9.410	1.00	32.97	RNA1 O
ATOM	2075	C1*	C C1076	5.735	18.385	-10.765	1.00	34.29	RNA1 C
ATOM	2076	N1	C C1076	6.012	16.945	-10.577	1.00	22.34	RNA1 N
ATOM	2077	C2	C C1076	5.036	16.150	-9.959	1.00	24.18	RNA1 C
ATOM	2078	O2	C C1076	3.977	16.680	-9.577	1.00	25.15	RNA1 O
ATOM	2079	N3	C C1076	5.271	14.825	-9.784	1.00	20.85	RNA1 N
ATOM	2080	C4	C C1076	6.428	14.295	-10.185	1.00	21.45	RNA1 C
ATOM	2081	N4	C C1076	6.611	12.987	-9.994	1.00	19.48	RNA1 N
ATOM	2082	C5	C C1076	7.446	15.083	-10.805	1.00	18.25	RNA1 C
ATOM	2083	C6	C C1076	7.196	16.389	-10.984	1.00	25.90	RNA1 C
ATOM	2084	P	A C1077	8.725	20.374	-7.602	1.00	34.53	RNA1 P
ATOM	2085	O1P	A C1077	9.776	19.366	-7.891	1.00	32.29	RNA1 O
ATOM	2086	O2P	A C1077	9.115	21.689	-7.025	1.00	55.02	RNA1 O
ATOM	2087	O5*	A C1077	7.641	19.691	-6.652	1.00	22.72	RNA1 O
ATOM	2088	C5*	A C1077	6.447	20.399	-6.283	1.00	17.11	RNA1 C
ATOM	2089	C4*	A C1077	5.461	19.477	-5.601	1.00	26.56	RNA1 C
ATOM	2090	O4*	A C1077	5.058	18.423	-6.514	1.00	34.54	RNA1 O
ATOM	2091	C3*	A C1077	5.916	18.724	-4.357	1.00	32.85	RNA1 C
ATOM	2092	O3*	A C1077	5.872	19.511	-3.175	1.00	37.36	RNA1 O
ATOM	2093	C2*	A C1077	4.913	17.576	-4.297	1.00	36.94	RNA1 C
ATOM	2094	O2*	A C1077	3.661	17.943	-3.748	1.00	32.73	RNA1 O
ATOM	2095	C1*	A C1077	4.723	17.255	-5.778	1.00	32.51	RNA1 C
ATOM	2096	N9	A C1077	5.612	16.160	-6.172	1.00	27.14	RNA1 N
ATOM	2097	C8	A C1077	6.830	16.224	-6.802	1.00	22.59	RNA1 C
ATOM	2098	N7	A C1077	7.406	15.054	-6.959	1.00	28.95	RNA1 N
ATOM	2099	C5	A C1077	6.500	14.158	-6.405	1.00	23.18	RNA1 C
ATOM	2100	C6	A C1077	6.524	12.758	-6.252	1.00	29.03	RNA1 C
ATOM	2101	N6	A C1077	7.543	11.984	-6.643	1.00	32.89	RNA1 N
ATOM	2102	N1	A C1077	5.454	12.174	-5.669	1.00	23.42	RNA1 N
ATOM	2103	C2	A C1077	4.443	12.948	-5.259	1.00	10.65	RNA1 C
ATOM	2104	N3	A C1077	4.309	14.266	-5.338	1.00	26.74	RNA1 N
ATOM	2105	C4	A C1077	5.385	14.821	-5.930	1.00	26.08	RNA1 C
ATOM	2106	P	U C1078	6.978	19.284	-2.026	1.00	29.17	RNA1 P
ATOM	2107	O1P	U C1078	8.330	19.420	-2.616	1.00	22.94	RNA1 O



ATOM	2108	O2P	U C1078	6.586	20.141	-0.877	1.00	41.57	RNA1 O
ATOM	2109	O5*	U C1078	6.828	17.754	-1.608	1.00	29.90	RNA1 O
ATOM	2110	C5*	U C1078	5.706	17.287	-0.830	1.00	21.78	RNA1 C
ATOM	2111	C4*	U C1078	5.789	15.785	-0.649	1.00	21.19	RNA1 C
ATOM	2112	O4*	U C1078	5.732	15.157	-1.957	1.00	29.99	RNA1 O
ATOM	2113	C3*	U C1078	7.075	15.241	-0.031	1.00	27.77	RNA1 C
ATOM	2114	O3*	U C1078	7.057	15.184	1.390	1.00	36.77	RNA1 O
ATOM	2115	C2*	U C1078	7.094	13.812	-0.554	1.00	34.85	RNA1 C
ATOM	2116	O2*	U C1078	6.229	12.972	0.191	1.00	32.65	RNA1 O
ATOM	2117	C1*	U C1078	6.532	13.986	-1.963	1.00	28.35	RNA1 C
ATOM	2118	N1	U C1078	7.611	14.137	-2.955	1.00	21.70	RNA1 N
ATOM	2119	C2	U C1078	8.275	12.987	-3.352	1.00	27.00	RNA1 C
ATOM	2120	O2	U C1078	7.975	11.872	-2.946	1.00	29.58	RNA1 O
ATOM	2121	N3	U C1078	9.305	13.189	-4.238	1.00	24.66	RNA1 N
ATOM	2122	C4	U C1078	9.728	14.393	-4.760	1.00	26.71	RNA1 C
ATOM	2123	O4	U C1078	10.714	14.417	-5.504	1.00	44.05	RNA1 O
ATOM	2124	C5	U C1078	8.978	15.530	-4.320	1.00	18.54	RNA1 C
ATOM	2125	C6	U C1078	7.970	15.368	-3.459	1.00	19.12	RNA1 C
ATOM	2126	P	C C1079	7.168	16.527	2.260	1.00	28.61	RNA1 P
ATOM	2127	O1P	C C1079	7.780	16.107	3.544	1.00	34.30	RNA1 O
ATOM	2128	O2P	C C1079	7.770	17.644	1.487	1.00	31.33	RNA1 O
ATOM	2129	O5*	C C1079	5.641	16.867	2.520	1.00	13.04	RNA1 O
ATOM	2130	C5*	C C1079	4.851	15.965	3.271	1.00	17.43	RNA1 C
ATOM	2131	C4*	C C1079	3.398	16.246	3.064	1.00	19.74	RNA1 C
ATOM	2132	O4*	C C1079	2.954	15.688	1.803	1.00	26.36	RNA1 O
ATOM	2133	C3*	C C1079	2.556	15.540	4.098	1.00	25.66	RNA1 C
ATOM	2134	O3*	C C1079	2.525	16.312	5.278	1.00	37.56	RNA1 O
ATOM	2135	C2*	C C1079	1.217	15.382	3.394	1.00	27.27	RNA1 C
ATOM	2136	O2*	C C1079	0.452	16.573	3.416	1.00	25.00	RNA1 O
ATOM	2137	C1*	C C1079	1.672	15.091	1.963	1.00	17.88	RNA1 C
ATOM	2138	N1	C C1079	1.795	13.641	1.677	1.00	17.52	RNA1 N
ATOM	2139	C2	C C1079	0.629	12.878	1.441	1.00	19.34	RNA1 C
ATOM	2140	O2	C C1079	-0.488	13.427	1.500	1.00	24.52	RNA1 O
ATOM	2141	N3	C C1079	0.748	11.561	1.159	1.00	15.18	RNA1 N
ATOM	2142	C4	C C1079	1.955	10.994	1.111	1.00	20.12	RNA1 C
ATOM	2143	N4	C C1079	2.018	9.691	0.814	1.00	14.62	RNA1 N
ATOM	2144	C5	C C1079	3.150	11.734	1.359	1.00	16.35	RNA1 C
ATOM	2145	C6	C C1079	3.025	13.040	1.635	1.00	14.99	RNA1 C
ATOM	2146	P	A C1080	2.747	15.593	6.692	1.00	32.18	RNA1 P
ATOM	2147	O1P	A C1080	3.901	14.668	6.598	1.00	27.65	RNA1 O
ATOM	2148	O2P	A C1080	2.748	16.674	7.711	1.00	42.21	RNA1 O
ATOM	2149	O5*	A C1080	1.413	14.745	6.853	1.00	24.30	RNA1 O
ATOM	2150	C5*	A C1080	0.157	15.421	6.836	1.00	25.92	RNA1 C
ATOM	2151	C4*	A C1080	-0.967	14.459	6.593	1.00	27.37	RNA1 C
ATOM	2152	O4*	A C1080	-0.902	13.924	5.248	1.00	35.15	RNA1 O



ATOM	2198	O2*	U C1082	-3.847	1.757	11.941	1.00	43.11	RNA1 O
ATOM	2199	C1*	U C1082	-3.000	3.510	10.496	1.00	29.73	RNA1 C
ATOM	2200	N1	U C1082	-1.691	4.146	10.281	1.00	21.48	RNA1 N
ATOM	2201	C2	U C1082	-0.650	3.342	9.826	1.00	24.74	RNA1 C
ATOM	2202	O2	U C1082	-0.781	2.155	9.573	1.00	35.44	RNA1 O
ATOM	2203	N3	U C1082	0.552	3.980	9.678	1.00	16.73	RNA1 N
ATOM	2204	C4	U C1082	0.825	5.303	9.921	1.00	20.16	RNA1 C
ATOM	2205	O4	U C1082	1.963	5.730	9.715	1.00	29.48	RNA1 O
ATOM	2206	C5	U C1082	-0.293	6.069	10.378	1.00	15.77	RNA1 C
ATOM	2207	C6	U C1082	-1.485	5.479	10.536	1.00	20.32	RNA1 C
ATOM	2208	P	U C1083	-3.685	3.548	15.138	1.00	44.11	RNA1 P
ATOM	2209	O1P	U C1083	-3.013	4.855	15.416	1.00	33.72	RNA1 O
ATOM	2210	O2P	U C1083	-4.550	2.923	16.170	1.00	44.56	RNA1 O
ATOM	2211	O5*	U C1083	-2.554	2.515	14.732	1.00	26.53	RNA1 O
ATOM	2212	C5*	U C1083	-1.204	2.710	15.133	1.00	27.01	RNA1 C
ATOM	2213	C4*	U C1083	-0.310	1.810	14.328	1.00	35.50	RNA1 C
ATOM	2214	O4*	U C1083	0.049	2.450	13.077	1.00	37.83	RNA1 O
ATOM	2215	C3*	U C1083	1.014	1.490	14.985	1.00	42.54	RNA1 C
ATOM	2216	O3*	U C1083	0.829	0.394	15.868	1.00	53.77	RNA1 O
ATOM	2217	C2*	U C1083	1.899	1.142	13.797	1.00	40.40	RNA1 C
ATOM	2218	O2*	U C1083	1.676	-0.184	13.354	1.00	50.14	RNA1 O
ATOM	2219	C1*	U C1083	1.383	2.112	12.733	1.00	31.81	RNA1 C
ATOM	2220	N1	U C1083	2.176	3.350	12.641	1.00	27.07	RNA1 N
ATOM	2221	C2	U C1083	3.403	3.291	11.995	1.00	27.98	RNA1 C
ATOM	2222	O2	U C1083	3.842	2.278	11.491	1.00	38.26	RNA1 O
ATOM	2223	N3	U C1083	4.101	4.471	11.959	1.00	27.06	RNA1 N
ATOM	2224	C4	U C1083	3.711	5.686	12.480	1.00	29.89	RNA1 C
ATOM	2225	O4	U C1083	4.463	6.660	12.376	1.00	35.97	RNA1 O
ATOM	2226	C5	U C1083	2.432	5.676	13.120	1.00	28.35	RNA1 C
ATOM	2227	C6	U C1083	1.726	4.538	13.180	1.00	34.18	RNA1 C
ATOM	2228	P	A C1084	1.531	0.409	17.308	1.00	46.22	RNA1 P
ATOM	2229	O1P	A C1084	1.502	1.811	17.819	1.00	47.82	RNA1 O
ATOM	2230	O2P	A C1084	0.915	-0.683	18.102	1.00	45.99	RNA1 O
ATOM	2231	O5*	A C1084	3.037	0.024	16.984	1.00	32.44	RNA1 O
ATOM	2232	C5*	A C1084	4.103	0.403	17.854	1.00	26.01	RNA1 C
ATOM	2233	C4*	A C1084	5.395	-0.104	17.293	1.00	30.31	RNA1 C
ATOM	2234	O4*	A C1084	5.314	-1.544	17.185	1.00	39.98	RNA1 O
ATOM	2235	C3*	A C1084	5.631	0.378	15.881	1.00	31.04	RNA1 C
ATOM	2236	O3*	A C1084	6.308	1.611	15.926	1.00	35.76	RNA1 O
ATOM	2237	C2*	A C1084	6.448	-0.741	15.252	1.00	34.39	RNA1 C
ATOM	2238	O2*	A C1084	7.825	-0.635	15.548	1.00	29.53	RNA1 O
ATOM	2239	C1*	A C1084	5.872	-1.970	15.956	1.00	36.40	RNA1 C
ATOM	2240	N9	A C1084	4.827	-2.698	15.230	1.00	38.88	RNA1 N
ATOM	2241	C8	A C1084	3.464	-2.577	15.388	1.00	38.21	RNA1 C
ATOM	2242	N7	A C1084	2.770	-3.432	14.677	1.00	33.92	RNA1 N

ATOM	2243	C5	A C1084	3.737	-4.151	13.984	1.00	35.92	RNA1 C
ATOM	2244	C6	A C1084	3.648	-5.222	13.069	1.00	34.35	RNA1 C
ATOM	2245	N6	A C1084	2.493	-5.781	12.695	1.00	38.02	RNA1 N
ATOM	2246	N1	A C1084	4.802	-5.704	12.551	1.00	36.24	RNA1 N
ATOM	2247	C2	A C1084	5.960	-5.145	12.935	1.00	38.72	RNA1 C
ATOM	2248	N3	A C1084	6.173	-4.143	13.790	1.00	34.15	RNA1 N
ATOM	2249	C4	A C1084	5.007	-3.689	14.291	1.00	36.93	RNA1 C
ATOM	2250	P	A C1085	5.839	2.793	14.965	1.00	32.91	RNA1 P
ATOM	2251	O1P	A C1085	4.351	2.768	14.939	1.00	23.95	RNA1 O
ATOM	2252	O2P	A C1085	6.554	4.030	15.366	1.00	36.15	RNA1 O
ATOM	2253	O5*	A C1085	6.414	2.342	13.557	1.00	34.02	RNA1 O
ATOM	2254	C5*	A C1085	7.826	2.172	13.384	1.00	35.68	RNA1 C
ATOM	2255	C4*	A C1085	8.100	1.383	12.136	1.00	40.49	RNA1 C
ATOM	2256	O4*	A C1085	7.592	0.035	12.283	1.00	46.64	RNA1 O
ATOM	2257	C3*	A C1085	7.426	1.921	10.889	1.00	37.28	RNA1 C
ATOM	2258	O3*	A C1085	8.249	2.933	10.322	1.00	38.08	RNA1 O
ATOM	2259	C2*	A C1085	7.311	0.685	10.002	1.00	36.45	RNA1 C
ATOM	2260	O2*	A C1085	8.496	0.425	9.278	1.00	44.66	RNA1 O
ATOM	2261	C1*	A C1085	7.122	-0.432	11.032	1.00	36.77	RNA1 C
ATOM	2262	N9	A C1085	5.743	-0.875	11.198	1.00	24.80	RNA1 N
ATOM	2263	C8	A C1085	4.754	-0.265	11.923	1.00	28.92	RNA1 C
ATOM	2264	N7	A C1085	3.606	-0.896	11.888	1.00	28.93	RNA1 N
ATOM	2265	C5	A C1085	3.857	-2.000	11.087	1.00	22.34	RNA1 C
ATOM	2266	C6	A C1085	3.040	-3.060	10.664	1.00	26.52	RNA1 C
ATOM	2267	N6	A C1085	1.749	-3.175	11.000	1.00	26.24	RNA1 N
ATOM	2268	N1	A C1085	3.596	-4.006	9.874	1.00	25.01	RNA1 N
ATOM	2269	C2	A C1085	4.889	-3.875	9.532	1.00	27.90	RNA1 C
ATOM	2270	N3	A C1085	5.758	-2.920	9.864	1.00	23.94	RNA1 N
ATOM	2271	C4	A C1085	5.171	-2.002	10.654	1.00	23.81	RNA1 C
ATOM	2272	P	A C1086	7.578	4.220	9.636	1.00	38.44	RNA1 P
ATOM	2273	O1P	A C1086	6.238	4.440	10.244	1.00	21.00	RNA1 O
ATOM	2274	O2P	A C1086	8.578	5.315	9.641	1.00	32.04	RNA1 O
ATOM	2275	O5*	A C1086	7.359	3.750	8.133	1.00	44.64	RNA1 O
ATOM	2276	C5*	A C1086	8.465	3.286	7.337	1.00	27.97	RNA1 C
ATOM	2277	C4*	A C1086	7.965	2.407	6.217	1.00	34.03	RNA1 C
ATOM	2278	O4*	A C1086	7.509	1.138	6.753	1.00	34.69	RNA1 O
ATOM	2279	C3*	A C1086	6.759	2.929	5.455	1.00	38.31	RNA1 C
ATOM	2280	O3*	A C1086	7.095	3.913	4.484	1.00	30.65	RNA1 O
ATOM	2281	C2*	A C1086	6.166	1.659	4.850	1.00	40.89	RNA1 C
ATOM	2282	O2*	A C1086	6.734	1.284	3.610	1.00	37.38	RNA1 O
ATOM	2283	C1*	A C1086	6.488	0.616	5.925	1.00	29.88	RNA1 C
ATOM	2284	N9	A C1086	5.326	0.253	6.739	1.00	26.28	RNA1 N
ATOM	2285	C8	A C1086	4.885	-1.015	7.018	1.00	26.71	RNA1 C
ATOM	2286	N7	A C1086	3.748	-1.049	7.675	1.00	32.50	RNA1 N
ATOM	2287	C5	A C1086	3.437	0.289	7.869	1.00	23.83	RNA1 C

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ATOM	2333	C6	A C1088	0.578	12.406	-2.033	1.00	14.84	RNA1 C
ATOM	2334	N6	A C1088	-0.708	12.768	-1.988	1.00	13.38	RNA1 N
ATOM	2335	N1	A C1088	1.517	13.309	-1.680	1.00	16.35	RNA1 N
ATOM	2336	C2	A C1088	2.807	12.952	-1.736	1.00	16.68	RNA1 C
ATOM	2337	N3	A C1088	3.343	11.792	-2.099	1.00	19.47	RNA1 N
ATOM	2338	C4	A C1088	2.383	10.917	-2.440	1.00	11.60	RNA1 C
ATOM	2339	P	G C1089	7.282	7.896	-5.216	1.00	26.48	RNA1 P
ATOM	2340	O1P	G C1089	7.768	9.270	-5.525	1.00	30.79	RNA1 O
ATOM	2341	O2P	G C1089	6.437	7.171	-6.198	1.00	18.45	RNA1 O
ATOM	2342	O5*	G C1089	8.548	7.011	-4.853	1.00	14.93	RNA1 O
ATOM	2343	C5*	G C1089	9.568	7.515	-3.971	1.00	29.50	RNA1 C
ATOM	2344	C4*	G C1089	10.362	6.367	-3.400	1.00	26.25	RNA1 C
ATOM	2345	O4*	G C1089	9.469	5.554	-2.600	1.00	34.26	RNA1 O
ATOM	2346	C3*	G C1089	10.981	5.439	-4.439	1.00	20.63	RNA1 C
ATOM	2347	O3*	G C1089	12.197	4.922	-3.925	1.00	28.79	RNA1 O
ATOM	2348	C2*	G C1089	9.965	4.305	-4.531	1.00	28.82	RNA1 C
ATOM	2349	O2*	G C1089	10.543	3.072	-4.908	1.00	40.76	RNA1 O
ATOM	2350	C1*	G C1089	9.439	4.238	-3.099	1.00	19.76	RNA1 C
ATOM	2351	N9	G C1089	8.069	3.749	-2.988	1.00	15.09	RNA1 N
ATOM	2352	C8	G C1089	6.930	4.499	-2.817	1.00	17.24	RNA1 C
ATOM	2353	N7	G C1089	5.848	3.773	-2.729	1.00	20.25	RNA1 N
ATOM	2354	C5	G C1089	6.301	2.466	-2.857	1.00	14.36	RNA1 C
ATOM	2355	C6	G C1089	5.590	1.243	-2.839	1.00	23.53	RNA1 C
ATOM	2356	O6	G C1089	4.368	1.060	-2.704	1.00	38.04	RNA1 O
ATOM	2357	N1	G C1089	6.442	0.156	-2.998	1.00	10.56	RNA1 N
ATOM	2358	C2	G C1089	7.801	0.235	-3.159	1.00	16.75	RNA1 C
ATOM	2359	N2	G C1089	8.456	-0.931	-3.305	1.00	18.05	RNA1 N
ATOM	2360	N3	G C1089	8.475	1.369	-3.178	1.00	14.70	RNA1 N
ATOM	2361	C4	G C1089	7.668	2.437	-3.022	1.00	10.92	RNA1 C
ATOM	2362	P	U C1090	13.585	5.675	-4.221	1.00	43.14	RNA1 P
ATOM	2363	O1P	U C1090	13.436	6.453	-5.476	1.00	42.35	RNA1 O
ATOM	2364	O2P	U C1090	14.010	6.371	-2.971	1.00	42.92	RNA1 O
ATOM	2365	O5*	U C1090	14.587	4.467	-4.490	1.00	39.62	RNA1 O
ATOM	2366	C5*	U C1090	15.989	4.585	-4.207	1.00	45.78	RNA1 C
ATOM	2367	C4*	U C1090	16.693	3.275	-4.492	1.00	55.27	RNA1 C
ATOM	2368	O4*	U C1090	16.237	2.246	-3.570	1.00	55.21	RNA1 O
ATOM	2369	C3*	U C1090	16.455	2.661	-5.862	1.00	53.66	RNA1 C
ATOM	2370	O3*	U C1090	17.267	3.222	-6.875	1.00	51.89	RNA1 O
ATOM	2371	C2*	U C1090	16.781	1.194	-5.637	1.00	48.18	RNA1 C
ATOM	2372	O2*	U C1090	18.172	0.949	-5.690	1.00	54.31	RNA1 O
ATOM	2373	C1*	U C1090	16.271	0.979	-4.213	1.00	41.15	RNA1 C
ATOM	2374	N1	U C1090	14.922	0.387	-4.190	1.00	41.07	RNA1 N
ATOM	2375	C2	U C1090	14.823	-0.998	-4.283	1.00	36.51	RNA1 C
ATOM	2376	O2	U C1090	15.792	-1.730	-4.388	1.00	37.99	RNA1 O
ATOM	2377	N3	U C1090	13.542	-1.493	-4.256	1.00	24.06	RNA1 N

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ATOM	2378	C4	U C1090	12.374	-0.772	-4.150	1.00	29.36	RNA1 C
ATOM	2379	O4	U C1090	11.297	-1.373	-4.078	1.00	32.44	RNA1 O
ATOM	2380	C5	U C1090	12.554	0.649	-4.068	1.00	27.73	RNA1 C
ATOM	2381	C6	U C1090	13.788	1.167	-4.087	1.00	33.24	RNA1 C
ATOM	2382	P	G C1091	16.725	3.245	-8.383	1.00	58.06	RNA1 P
ATOM	2383	O1P	G C1091	15.277	3.599	-8.351	1.00	49.18	RNA1 O
ATOM	2384	O2P	G C1091	17.668	4.074	-9.177	1.00	62.85	RNA1 O
ATOM	2385	O5*	G C1091	16.838	1.724	-8.851	1.00	59.36	RNA1 O
ATOM	2386	C5*	G C1091	18.123	1.141	-9.135	1.00	62.76	RNA1 C
ATOM	2387	C4*	G C1091	18.029	-0.370	-9.212	1.00	62.76	RNA1 C
ATOM	2388	O4*	G C1091	17.448	-0.882	-7.980	1.00	57.83	RNA1 O
ATOM	2389	C3*	G C1091	17.168	-0.998	-10.302	1.00	67.15	RNA1 C
ATOM	2390	O3*	G C1091	17.800	-1.073	-11.581	1.00	73.47	RNA1 O
ATOM	2391	C2*	G C1091	16.911	-2.391	-9.736	1.00	63.68	RNA1 C
ATOM	2392	O2*	G C1091	17.997	-3.276	-9.939	1.00	66.38	RNA1 O
ATOM	2393	C1*	G C1091	16.766	-2.098	-8.243	1.00	52.76	RNA1 C
ATOM	2394	N9	G C1091	15.354	-1.954	-7.902	1.00	42.68	RNA1 N
ATOM	2395	C8	G C1091	14.638	-0.795	-7.717	1.00	43.79	RNA1 C
ATOM	2396	N7	G C1091	13.368	-1.009	-7.490	1.00	42.36	RNA1 N
ATOM	2397	C5	G C1091	13.243	-2.392	-7.512	1.00	31.07	RNA1 C
ATOM	2398	C6	G C1091	12.100	-3.220	-7.342	1.00	32.80	RNA1 C
ATOM	2399	O6	G C1091	10.926	-2.886	-7.133	1.00	29.29	RNA1 O
ATOM	2400	N1	G C1091	12.427	-4.567	-7.442	1.00	27.53	RNA1 N
ATOM	2401	C2	G C1091	13.687	-5.057	-7.676	1.00	37.58	RNA1 C
ATOM	2402	N2	G C1091	13.806	-6.387	-7.734	1.00	43.37	RNA1 N
ATOM	2403	N3	G C1091	14.754	-4.300	-7.840	1.00	37.83	RNA1 N
ATOM	2404	C4	G C1091	14.461	-2.989	-7.748	1.00	34.74	RNA1 C
ATOM	2405	P	C C1092	16.901	-1.334	-12.902	1.00	78.16	RNA1 P
ATOM	2406	O1P	C C1092	15.717	-0.429	-12.869	1.00	76.90	RNA1 O
ATOM	2407	O2P	C C1092	17.813	-1.307	-14.079	1.00	77.44	RNA1 O
ATOM	2408	O5*	C C1092	16.360	-2.822	-12.721	1.00	69.64	RNA1 O
ATOM	2409	C5*	C C1092	17.277	-3.929	-12.693	1.00	63.11	RNA1 C
ATOM	2410	C4*	C C1092	16.536	-5.243	-12.604	1.00	59.28	RNA1 C
ATOM	2411	O4*	C C1092	15.859	-5.364	-11.322	1.00	50.31	RNA1 O
ATOM	2412	C3*	C C1092	15.433	-5.487	-13.621	1.00	60.54	RNA1 C
ATOM	2413	O3*	C C1092	15.910	-5.898	-14.893	1.00	61.03	RNA1 O
ATOM	2414	C2*	C C1092	14.614	-6.580	-12.949	1.00	56.00	RNA1 C
ATOM	2415	O2*	C C1092	15.155	-7.875	-13.128	1.00	59.60	RNA1 O
ATOM	2416	C1*	C C1092	14.704	-6.175	-11.477	1.00	46.68	RNA1 C
ATOM	2417	N1	C C1092	13.500	-5.411	-11.103	1.00	45.69	RNA1 N
ATOM	2418	C2	C C1092	12.311	-6.125	-10.845	1.00	48.75	RNA1 C
ATOM	2419	O2	C C1092	12.334	-7.367	-10.877	1.00	35.22	RNA1 O
ATOM	2420	N3	C C1092	11.175	-5.443	-10.568	1.00	40.06	RNA1 N
ATOM	2421	C4	C C1092	11.191	-4.109	-10.529	1.00	43.65	RNA1 C
ATOM	2422	N4	C C1092	10.043	-3.483	-10.269	1.00	38.14	RNA1 N

ATOM	2423	C5	C C1092	12.386	-3.357	-10.759	1.00	43.83	RNA1 C
ATOM	2424	C6	C C1092	13.508	-4.043	-11.036	1.00	48.70	RNA1 C
ATOM	2425	P	G C1093	15.082	-5.497	-16.210	1.00	59.69	RNA1 P
ATOM	2426	O1P	G C1093	14.954	-4.014	-16.213	1.00	64.26	RNA1 O
ATOM	2427	O2P	G C1093	15.706	-6.182	-17.376	1.00	68.36	RNA1 O
ATOM	2428	O5*	G C1093	13.629	-6.109	-15.961	1.00	39.18	RNA1 O
ATOM	2429	C5*	G C1093	13.440	-7.525	-15.810	1.00	34.94	RNA1 C
ATOM	2430	C4*	G C1093	12.017	-7.828	-15.395	1.00	40.12	RNA1 C
ATOM	2431	O4*	G C1093	11.737	-7.199	-14.117	1.00	45.67	RNA1 O
ATOM	2432	C3*	G C1093	10.929	-7.304	-16.315	1.00	43.53	RNA1 C
ATOM	2433	O3*	G C1093	10.687	-8.168	-17.410	1.00	48.03	RNA1 O
ATOM	2434	C2*	G C1093	9.720	-7.183	-15.391	1.00	41.69	RNA1 C
ATOM	2435	O2*	G C1093	8.996	-8.389	-15.229	1.00	27.92	RNA1 O
ATOM	2436	C1*	G C1093	10.381	-6.769	-14.075	1.00	38.16	RNA1 C
ATOM	2437	N9	G C1093	10.350	-5.318	-13.870	1.00	36.77	RNA1 N
ATOM	2438	C8	G C1093	11.401	-4.431	-13.970	1.00	34.83	RNA1 C
ATOM	2439	N7	G C1093	11.048	-3.190	-13.762	1.00	32.06	RNA1 N
ATOM	2440	C5	G C1093	9.685	-3.259	-13.505	1.00	27.72	RNA1 C
ATOM	2441	C6	G C1093	8.752	-2.231	-13.223	1.00	27.54	RNA1 C
ATOM	2442	O6	G C1093	8.947	-1.013	-13.160	1.00	34.45	RNA1 O
ATOM	2443	N1	G C1093	7.475	-2.743	-13.014	1.00	19.53	RNA1 N
ATOM	2444	C2	G C1093	7.136	-4.075	-13.075	1.00	19.64	RNA1 C
ATOM	2445	N2	G C1093	5.851	-4.382	-12.830	1.00	17.24	RNA1 N
ATOM	2446	N3	G C1093	7.993	-5.040	-13.352	1.00	21.92	RNA1 N
ATOM	2447	C4	G C1093	9.241	-4.566	-13.554	1.00	25.99	RNA1 C
ATOM	2448	P	U C1094	10.214	-7.545	-18.808	1.00	48.86	RNA1 P
ATOM	2449	O1P	U C1094	11.019	-6.314	-19.033	1.00	51.40	RNA1 O
ATOM	2450	O2P	U C1094	10.225	-8.631	-19.820	1.00	62.99	RNA1 O
ATOM	2451	O5*	U C1094	8.700	-7.137	-18.549	1.00	35.14	RNA1 O
ATOM	2452	C5*	U C1094	7.726	-8.151	-18.319	1.00	39.65	RNA1 C
ATOM	2453	C4*	U C1094	6.342	-7.561	-18.289	1.00	45.60	RNA1 C
ATOM	2454	O4*	U C1094	6.086	-6.907	-17.022	1.00	47.84	RNA1 O
ATOM	2455	C3*	U C1094	6.030	-6.503	-19.328	1.00	46.03	RNA1 C
ATOM	2456	O3*	U C1094	5.775	-7.078	-20.601	1.00	56.79	RNA1 O
ATOM	2457	C2*	U C1094	4.829	-5.786	-18.713	1.00	44.04	RNA1 C
ATOM	2458	O2*	U C1094	3.588	-6.431	-18.943	1.00	37.76	RNA1 O
ATOM	2459	C1*	U C1094	5.168	-5.844	-17.219	1.00	44.47	RNA1 C
ATOM	2460	N1	U C1094	5.770	-4.589	-16.742	1.00	26.87	RNA1 N
ATOM	2461	C2	U C1094	4.909	-3.585	-16.329	1.00	22.09	RNA1 C
ATOM	2462	O2	U C1094	3.691	-3.719	-16.288	1.00	25.93	RNA1 O
ATOM	2463	N3	U C1094	5.519	-2.419	-15.962	1.00	13.38	RNA1 N
ATOM	2464	C4	U C1094	6.869	-2.159	-15.947	1.00	36.16	RNA1 C
ATOM	2465	O4	U C1094	7.263	-1.036	-15.621	1.00	36.16	RNA1 O
ATOM	2466	C5	U C1094	7.696	-3.256	-16.357	1.00	27.39	RNA1 C
ATOM	2467	C6	U C1094	7.131	-4.404	-16.729	1.00	19.00	RNA1 C



ATOM	2468	P	A C1095	6.404	-6.394	-21.913	1.00	56.22	RNA1 P
ATOM	2469	O1P	A C1095	7.761	-5.866	-21.571	1.00	36.24	RNA1 O
ATOM	2470	O2P	A C1095	6.257	-7.345	-23.045	1.00	62.45	RNA1 O
ATOM	2471	O5*	A C1095	5.420	-5.169	-22.156	1.00	37.34	RNA1 O
ATOM	2472	C5*	A C1095	5.858	-3.993	-22.836	1.00	26.88	RNA1 C
ATOM	2473	C4*	A C1095	4.732	-3.002	-22.897	1.00	25.01	RNA1 C
ATOM	2474	O4*	A C1095	3.576	-3.668	-23.451	1.00	31.13	RNA1 O
ATOM	2475	C3*	A C1095	4.254	-2.489	-21.555	1.00	30.12	RNA1 C
ATOM	2476	O3*	A C1095	5.068	-1.403	-21.134	1.00	47.22	RNA1 O
ATOM	2477	C2*	A C1095	2.797	-2.116	-21.824	1.00	32.85	RNA1 C
ATOM	2478	O2*	A C1095	2.630	-0.839	-22.418	1.00	29.79	RNA1 O
ATOM	2479	C1*	A C1095	2.395	-3.179	-22.845	1.00	21.93	RNA1 C
ATOM	2480	N9	A C1095	1.649	-4.328	-22.333	1.00	17.01	RNA1 N
ATOM	2481	C8	A C1095	2.142	-5.568	-21.985	1.00	21.36	RNA1 C
ATOM	2482	N7	A C1095	1.211	-6.424	-21.627	1.00	21.32	RNA1 N
ATOM	2483	C5	A C1095	0.031	-5.696	-21.729	1.00	10.86	RNA1 C
ATOM	2484	C6	A C1095	-1.315	-6.037	-21.498	1.00	23.82	RNA1 C
ATOM	2485	N6	A C1095	-1.717	-7.254	-21.118	1.00	35.80	RNA1 N
ATOM	2486	N1	A C1095	-2.249	-5.076	-21.679	1.00	30.20	RNA1 N
ATOM	2487	C2	A C1095	-1.844	-3.861	-22.076	1.00	23.15	RNA1 C
ATOM	2488	N3	A C1095	-0.610	-3.423	-22.337	1.00	20.47	RNA1 N
ATOM	2489	C4	A C1095	0.289	-4.399	-22.143	1.00	9.00	RNA1 C
ATOM	2490	P	A C1096	5.554	-1.325	-19.607	1.00	33.71	RNA1 P
ATOM	2491	O1P	A C1096	5.985	-2.689	-19.209	1.00	38.06	RNA1 O
ATOM	2492	O2P	A C1096	6.505	-0.198	-19.472	1.00	30.42	RNA1 O
ATOM	2493	O5*	A C1096	4.203	-0.950	-18.856	1.00	19.71	RNA1 O
ATOM	2494	C5*	A C1096	3.610	0.332	-19.065	1.00	17.59	RNA1 C
ATOM	2495	C4*	A C1096	2.176	0.335	-18.609	1.00	25.20	RNA1 C
ATOM	2496	O4*	A C1096	1.399	-0.548	-19.452	1.00	36.18	RNA1 O
ATOM	2497	C3*	A C1096	1.916	-0.155	-17.197	1.00	31.52	RNA1 C
ATOM	2498	O3*	A C1096	2.158	0.858	-16.224	1.00	40.13	RNA1 O
ATOM	2499	C2*	A C1096	0.458	-0.589	-17.277	1.00	29.94	RNA1 C
ATOM	2500	O2*	A C1096	-0.436	0.497	-17.220	1.00	33.53	RNA1 O
ATOM	2501	C1*	A C1096	0.392	-1.181	-18.684	1.00	28.76	RNA1 C
ATOM	2502	N9	A C1096	0.682	-2.615	-18.662	1.00	29.57	RNA1 N
ATOM	2503	C8	A C1096	1.915	-3.230	-18.760	1.00	20.07	RNA1 C
ATOM	2504	N7	A C1096	1.862	-4.536	-18.673	1.00	16.60	RNA1 N
ATOM	2505	C5	A C1096	0.506	-4.803	-18.515	1.00	21.73	RNA1 C
ATOM	2506	C6	A C1096	-0.207	-6.004	-18.372	1.00	21.62	RNA1 C
ATOM	2507	N6	A C1096	0.376	-7.207	-18.386	1.00	30.29	RNA1 N
ATOM	2508	N1	A C1096	-1.551	-5.928	-18.222	1.00	19.53	RNA1 N
ATOM	2509	C2	A C1096	-2.130	-4.715	-18.234	1.00	19.83	RNA1 C
ATOM	2510	N3	A C1096	-1.565	-3.512	-18.377	1.00	21.31	RNA1 N
ATOM	2511	C4	A C1096	-0.231	-3.630	-18.511	1.00	13.07	RNA1 C
ATOM	2512	P	C C1097	2.770	0.451	-14.795	1.00	34.58	RNA1 P

ATOM	2513	O1P	C C1097	3.901	-0.488	-15.013	1.00	24.95	RNA1 O
ATOM	2514	O2P	C C1097	3.010	1.716	-14.062	1.00	42.37	RNA1 O
ATOM	2515	O5*	C C1097	1.558	-0.333	-14.115	1.00	33.44	RNA1 O
ATOM	2516	C5*	C C1097	1.711	-1.664	-13.564	1.00	27.30	RNA1 C
ATOM	2517	C4*	C C1097	0.347	-2.298	-13.386	1.00	34.16	RNA1 C
ATOM	2518	O4*	C C1097	-0.067	-2.943	-14.625	1.00	37.39	RNA1 O
ATOM	2519	C3*	C C1097	0.219	-3.406	-12.354	1.00	33.88	RNA1 C
ATOM	2520	O3*	C C1097	0.093	-2.924	-11.025	1.00	36.37	RNA1 O
ATOM	2521	C2*	C C1097	-1.041	-4.120	-12.816	1.00	36.19	RNA1 C
ATOM	2522	O2*	C C1097	-2.214	-3.415	-12.457	1.00	31.86	RNA1 O
ATOM	2523	C1*	C C1097	-0.865	-4.089	-14.334	1.00	35.36	RNA1 C
ATOM	2524	N1	C C1097	-0.146	-5.311	-14.780	1.00	29.78	RNA1 N
ATOM	2525	C2	C C1097	-0.859	-6.537	-14.895	1.00	31.29	RNA1 C
ATOM	2526	O2	C C1097	-2.097	-6.552	-14.732	1.00	30.74	RNA1 O
ATOM	2527	N3	C C1097	-0.175	-7.667	-15.188	1.00	27.52	RNA1 N
ATOM	2528	C4	C C1097	1.146	-7.616	-15.390	1.00	35.55	RNA1 C
ATOM	2529	N4	C C1097	1.788	-8.764	-15.640	1.00	38.53	RNA1 N
ATOM	2530	C5	C C1097	1.874	-6.389	-15.338	1.00	27.77	RNA1 C
ATOM	2531	C6	C C1097	1.197	-5.275	-15.036	1.00	24.47	RNA1 C
ATOM	2532	P	A C1098	1.072	-3.493	-9.886	1.00	38.47	RNA1 P
ATOM	2533	O1P	A C1098	2.477	-3.131	-10.212	1.00	22.01	RNA1 O
ATOM	2534	O2P	A C1098	0.484	-3.068	-8.588	1.00	56.40	RNA1 O
ATOM	2535	O5*	A C1098	0.959	-5.079	-10.023	1.00	40.54	RNA1 O
ATOM	2536	C5*	A C1098	-0.328	-5.740	-9.972	1.00	47.03	RNA1 C
ATOM	2537	C4*	A C1098	-0.192	-7.201	-10.348	1.00	50.05	RNA1 C
ATOM	2538	O4*	A C1098	0.276	-7.310	-11.720	1.00	43.04	RNA1 O
ATOM	2539	C3*	A C1098	0.819	-8.007	-9.544	1.00	59.35	RNA1 C
ATOM	2540	O3*	A C1098	0.289	-8.467	-8.305	1.00	57.94	RNA1 O
ATOM	2541	C2*	A C1098	1.170	-9.146	-10.496	1.00	54.42	RNA1 C
ATOM	2542	O2*	A C1098	0.229	-10.203	-10.479	1.00	63.88	RNA1 O
ATOM	2543	C1*	A C1098	1.125	-8.440	-11.851	1.00	42.41	RNA1 C
ATOM	2544	N9	A C1098	2.456	-7.982	-12.247	1.00	29.98	RNA1 N
ATOM	2545	C8	A C1098	2.967	-6.709	-12.213	1.00	32.72	RNA1 C
ATOM	2546	N7	A C1098	4.222	-6.633	-12.588	1.00	34.32	RNA1 N
ATOM	2547	C5	A C1098	4.557	-7.942	-12.902	1.00	34.44	RNA1 C
ATOM	2548	C6	A C1098	5.751	-8.533	-13.363	1.00	43.55	RNA1 C
ATOM	2549	N6	A C1098	6.879	-7.852	-13.597	1.00	39.58	RNA1 N
ATOM	2550	N1	A C1098	5.746	-9.866	-13.579	1.00	48.91	RNA1 N
ATOM	2551	C2	A C1098	4.615	-10.549	-13.348	1.00	42.95	RNA1 C
ATOM	2552	N3	A C1098	3.435	-10.108	-12.916	1.00	35.82	RNA1 N
ATOM	2553	C4	A C1098	3.474	-8.782	-12.708	1.00	35.65	RNA1 C
ATOM	2554	P	G C1099	1.238	-8.516	-7.006	1.00	52.26	RNA1 P
ATOM	2555	O1P	G C1099	1.696	-7.137	-6.706	1.00	52.99	RNA1 O
ATOM	2556	O2P	G C1099	0.511	-9.287	-5.970	1.00	54.62	RNA1 O
ATOM	2557	O5*	G C1099	2.513	-9.346	-7.481	1.00	43.47	RNA1 O

ATOM	2558	C5*	G C1099	2.413	-10.749	-7.772	1.00	41.68	RNA1 C
ATOM	2559	C4*	G C1099	3.735	-11.273	-8.271	1.00	42.05	RNA1 C
ATOM	2560	O4*	G C1099	4.033	-10.671	-9.554	1.00	43.83	RNA1 O
ATOM	2561	C3*	G C1099	4.938	-10.934	-7.409	1.00	48.09	RNA1 C
ATOM	2562	O3*	G C1099	5.100	-11.821	-6.317	1.00	58.27	RNA1 O
ATOM	2563	C2*	G C1099	6.089	-10.992	-8.402	1.00	50.43	RNA1 C
ATOM	2564	O2*	G C1099	6.588	-12.296	-8.639	1.00	57.02	RNA1 O
ATOM	2565	C1*	G C1099	5.426	-10.432	-9.660	1.00	44.89	RNA1 C
ATOM	2566	N9	G C1099	5.639	-8.989	-9.729	1.00	45.65	RNA1 N
ATOM	2567	C8	G C1099	4.714	-7.993	-9.515	1.00	38.56	RNA1 C
ATOM	2568	N7	G C1099	5.228	-6.796	-9.584	1.00	41.94	RNA1 N
ATOM	2569	C5	G C1099	6.569	-7.014	-9.873	1.00	34.92	RNA1 C
ATOM	2570	C6	G C1099	7.631	-6.094	-10.053	1.00	42.48	RNA1 C
ATOM	2571	O6	G C1099	7.601	-4.857	-9.985	1.00	44.46	RNA1 O
ATOM	2572	N1	G C1099	8.829	-6.746	-10.336	1.00	41.82	RNA1 N
ATOM	2573	C2	G C1099	8.982	-8.108	-10.437	1.00	42.77	RNA1 C
ATOM	2574	N2	G C1099	10.211	-8.548	-10.736	1.00	31.50	RNA1 N
ATOM	2575	N3	G C1099	8.001	-8.974	-10.262	1.00	31.12	RNA1 N
ATOM	2576	C4	G C1099	6.832	-8.362	-9.984	1.00	33.36	RNA1 C
ATOM	2577	P	CC1100	5.772	-11.286	-4.956	1.00	62.31	RNA1 P
ATOM	2578	O1P	..C C1100	5.270	-9.914	-4.687	1.00	56.23	RNA1 O
ATOM	2579	O2P	C C1100	5.583	-12.348	-3.934	1.00	65.10	RNA1 O
ATOM	2580	O5*	C C1100	7.320	-11.188	-5.316	1.00	45.54	RNA1 O
ATOM	2581	C5*	C C1100	8.052	-12.366	-5.670	1.00	43.72	RNA1 C
ATOM	2582	C4*	C C1100	9.458	-12.015	-6.069	1.00	40.97	RNA1 C
ATOM	2583	O4*	C C1100	9.429	-11.213	-7.276	1.00	44.70	RNA1 O
ATOM	2584	C3*	C C1100	10.249	-11.173	-5.087	1.00	43.30	RNA1 C
ATOM	2585	O3*	C C1100	10.817	-11.913	-4.022	1.00	57.32	RNA1 O
ATOM	2586	C2*	C C1100	11.306	-10.543	-5.980	1.00	45.40	RNA1 C
ATOM	2587	O2*	C C1100	12.407	-11.390	-6.236	1.00	41.08	RNA1 O
ATOM	2588	C1*	C C1100	10.508	-10.293	-7.258	1.00	40.42	RNA1 C
ATOM	2589	N1	C C1100	9.968	-8.923	-7.239	1.00	34.22	RNA1 N
ATOM	2590	C2	C C1100	10.851	-7.860	-7.450	1.00	34.09	RNA1 C
ATOM	2591	O2	C C1100	12.043	-8.112	-7.698	1.00	30.44	RNA1 O
ATOM	2592	N3	C C1100	10.390	-6.595	-7.377	1.00	32.20	RNA1 N
ATOM	2593	C4	C C1100	9.102	-6.369	-7.112	1.00	36.06	RNA1 C
ATOM	2594	N4	C C1100	8.695	-5.101	-7.023	1.00	42.37	RNA1 N
ATOM	2595	C5	C C1100	8.173	-7.432	-6.920	1.00	31.00	RNA1 C
ATOM	2596	C6	C C1100	8.643	-8.681	-6.995	1.00	29.98	RNA1 C
ATOM	2597	P	UC1101	11.026	-11.199	-2.592	1.00	60.70	RNA1 P
ATOM	2598	O1P	U C1101	9.727	-10.588	-2.196	1.00	50.26	RNA1 O
ATOM	2599	O2P	U C1101	11.694	-12.160	-1.673	1.00	70.90	RNA1 O
ATOM	2600	O5*	U C1101	12.055	-10.024	-2.904	1.00	44.87	RNA1 O
ATOM	2601	C5*	U C1101	13.364	-10.316	-3.411	1.00	39.54	RNA1 C
ATOM	2602	C4*	U C1101	14.139	-9.041	-3.619	1.00	45.93	RNA1 C

ATOM	2603	O4*	U	C1101	13.487	-8.234	-4.635	1.00	53.56	RNA1	O
ATOM	2604	C3*	U	C1101	14.232	-8.111	-2.424	1.00	45.04	RNA1	C
ATOM	2605	O3*	U	C1101	15.241	-8.491	-1.503	1.00	55.35	RNA1	O
ATOM	2606	C2*	U	C1101	14.519	-6.767	-3.078	1.00	45.97	RNA1	C
ATOM	2607	O2*	U	C1101	15.875	-6.620	-3.450	1.00	43.86	RNA1	O
ATOM	2608	C1*	U	C1101	13.668	-6.856	-4.341	1.00	43.43	RNA1	C
ATOM	2609	N1	U	C1101	12.349	-6.220	-4.172	1.00	40.87	RNA1	N
ATOM	2610	C2	U	C1101	12.289	-4.831	-4.234	1.00	35.67	RNA1	C
ATOM	2611	O2	U	C1101	13.277	-4.130	-4.420	1.00	34.43	RNA1	O
ATOM	2612	N3	U	C1101	11.032	-4.294	-4.067	1.00	27.89	RNA1	N
ATOM	2613	C4	U	C1101	9.851	-4.983	-3.852	1.00	38.34	RNA1	C
ATOM	2614	O4	U	C1101	8.792	-4.355	-3.727	1.00	30.79	RNA1	O
ATOM	2615	C5	U	C1101	9.993	-6.408	-3.801	1.00	38.67	RNA1	C
ATOM	2616	C6	U	C1101	11.204	-6.965	-3.959	1.00	40.99	RNA1	C
ATOM	2617	P	C	C1102	15.110	-8.040	0.038	1.00	56.93	RNA1	P
ATOM	2618	O1P	C	C1102	13.690	-8.220	0.458	1.00	45.32	RNA1	O
ATOM	2619	O2P	C	C1102	16.195	-8.697	0.810	1.00	59.07	RNA1	O
ATOM	2620	O5*	C	C1102	15.415	-6.479	0.002	1.00	47.10	RNA1	O
ATOM	2621	C5*	C	C1102	16.687	-6.002	-0.447	1.00	40.92	RNA1	C
ATOM	2622	C4*	C	C1102	16.706	-4.495	-0.480	1.00	41.54	RNA1	C
ATOM	2623	O4*	C	C1102	15.809	-4.001	-1.511	1.00	45.86	RNA1	O
ATOM	2624	C3*	C	C1102	16.235	-3.772	0.769	1.00	43.22	RNA1	C
ATOM	2625	O3*	C	C1102	17.189	-3.732	1.814	1.00	49.70	RNA1	O
ATOM	2626	C2*	C	C1102	15.910	-2.389	0.227	1.00	45.44	RNA1	C
ATOM	2627	O2*	C	C1102	17.061	-1.587	0.031	1.00	39.52	RNA1	O
ATOM	2628	C1*	C	C1102	15.294	-2.733	-1.125	1.00	41.32	RNA1	C
ATOM	2629	N1	C	C1102	13.822	-2.807	-1.006	1.00	35.07	RNA1	N
ATOM	2630	C2	C	C1102	13.091	-1.607	-0.999	1.00	35.73	RNA1	C
ATOM	2631	O2	C	C1102	13.700	-0.530	-1.134	1.00	40.70	RNA1	O
ATOM	2632	N3	C	C1102	11.748	-1.649	-0.843	1.00	24.21	RNA1	N
ATOM	2633	C4	C	C1102	11.131	-2.821	-0.703	1.00	25.56	RNA1	C
ATOM	2634	N4	C	C1102	9.805	-2.813	-0.534	1.00	27.04	RNA1	N
ATOM	2635	C5	C	C1102	11.844	-4.056	-0.726	1.00	25.22	RNA1	C
ATOM	2636	C6	C	C1102	13.175	-4.004	-0.880	1.00	29.24	RNA1	C
ATOM	2637	P	A	C1103	16.678	-3.598	3.336	1.00	46.37	RNA1	P
ATOM	2638	O1P	A	C1103	15.453	-4.431	3.507	1.00	34.79	RNA1	O
ATOM	2639	O2P	A	C1103	17.841	-3.806	4.238	1.00	53.23	RNA1	O
ATOM	2640	O5*	A	C1103	16.223	-2.077	3.443	1.00	50.88	RNA1	O
ATOM	2641	C5*	A	C1103	17.095	-1.012	3.017	1.00	45.92	RNA1	C
ATOM	2642	C4*	A	C1103	16.368	0.307	3.082	1.00	42.03	RNA1	C
ATOM	2643	O4*	A	C1103	15.249	0.282	2.164	1.00	42.45	RNA1	O
ATOM	2644	C3*	A	C1103	15.748	0.629	4.431	1.00	46.34	RNA1	C
ATOM	2645	O3*	A	C1103	16.697	1.231	5.297	1.00	50.61	RNA1	O
ATOM	2646	C2*	A	C1103	14.604	1.568	4.068	1.00	40.60	RNA1	C
ATOM	2647	O2*	A	C1103	15.018	2.911	3.913	1.00	43.99	RNA1	O

ATOM	2648	C1*	A C1103	14.163	1.007	2.714	1.00	35.23	RNA1 C
ATOM	2649	N9	A C1103	13.007	0.114	2.815	1.00	24.56	RNA1 N
ATOM	2650	C8	A C1103	12.964	-1.259	2.771	1.00	12.09	RNA1 C
ATOM	2651	N7	A C1103	11.755	-1.754	2.912	1.00	21.27	RNA1 N
ATOM	2652	C5	A C1103	10.949	-0.629	3.052	1.00	11.33	RNA1 C
ATOM	2653	C6	A C1103	9.566	-0.469	3.247	1.00	17.54	RNA1 C
ATOM	2654	N6	A C1103	8.699	-1.485	3.341	1.00	18.44	RNA1 N
ATOM	2655	N1	A C1103	9.091	0.792	3.351	1.00	23.77	RNA1 N
ATOM	2656	C2	A C1103	9.947	1.810	3.270	1.00	20.47	RNA1 C
ATOM	2657	N3	A C1103	11.262	1.789	3.093	1.00	25.40	RNA1 N
ATOM	2658	C4	A C1103	11.706	0.525	2.990	1.00	22.14	RNA1 C
ATOM	2659	P	C C1104	16.907	0.637	6.771	1.00	47.34	RNA1 P
ATOM	2660	O1P	C C1104	17.274	-0.801	6.656	1.00	47.39	RNA1 O
ATOM	2661	O2P	C C1104	17.809	1.572	7.493	1.00	49.59	RNA1 O
ATOM	2662	O5*	C C1104	15.454	0.717	7.410	1.00	32.80	RNA1 O
ATOM	2663	C5*	C C1104	14.847	1.985	7.660	1.00	32.89	RNA1 C
ATOM	2664	C4*	C C1104	13.409	1.804	8.055	1.00	33.67	RNA1 C
ATOM	2665	O4*	C C1104	12.654	1.301	6.924	1.00	36.61	RNA1 O
ATOM	2666	C3*	C C1104	13.151	0.793	9.157	1.00	44.60	RNA1 C
ATOM	2667	O3*	C C1104	13.379	1.321	10.455	1.00	47.83	RNA1 O
ATOM	2668	C2*	C C1104	11.699	0.409	8.912	1.00	41.50	RNA1 C
ATOM	2669	O2*	C C1104	10.802	1.363	9.443	1.00	39.51	RNA1 O
ATOM	2670	C1*	C C1104	11.635	0.426	7.382	1.00	35.38	RNA1 C
ATOM	2671	N1	C C1104	11.881	-0.915	6.818	1.00	26.79	RNA1 N
ATOM	2672	C2	C C1104	10.807	-1.804	6.699	1.00	30.49	RNA1 C
ATOM	2673	O2	C C1104	9.672	-1.426	7.039	1.00	25.17	RNA1 O
ATOM	2674	N3	C C1104	11.031	-3.049	6.216	1.00	35.06	RNA1 N
ATOM	2675	C4	C C1104	12.264	-3.412	5.850	1.00	35.48	RNA1 C
ATOM	2676	N4	C C1104	12.440	-4.649	5.381	1.00	39.73	RNA1 N
ATOM	2677	C5	C C1104	13.370	-2.524	5.948	1.00	26.28	RNA1 C
ATOM	2678	C6	C C1104	13.137	-1.298	6.432	1.00	26.38	RNA1 C
ATOM	2679	P	C C1105	13.943	0.357	11.610	1.00	45.15	RNA1 P
ATOM	2680	O1P	C C1105	14.937	-0.579	11.008	1.00	37.59	RNA1 O
ATOM	2681	O2P	C C1105	14.345	1.217	12.749	1.00	50.66	RNA1 O
ATOM	2682	O5*	C C1105	12.669	-0.496	12.036	1.00	27.84	RNA1 O
ATOM	2683	C5*	C C1105	11.541	0.141	12.636	1.00	26.44	RNA1 C
ATOM	2684	C4*	C C1105	10.431	-0.855	12.852	1.00	36.80	RNA1 C
ATOM	2685	O4*	C C1105	9.967	-1.354	11.569	1.00	46.02	RNA1 O
ATOM	2686	C3*	C C1105	10.793	-2.111	13.623	1.00	39.57	RNA1 C
ATOM	2687	O3*	C C1105	10.794	-1.905	15.026	1.00	48.60	RNA1 O
ATOM	2688	C2*	C C1105	9.713	-3.084	13.169	1.00	42.79	RNA1 C
ATOM	2689	O2*	C C1105	8.473	-2.848	13.811	1.00	36.52	RNA1 O
ATOM	2690	C1*	C C1105	9.576	-2.714	11.693	1.00	39.01	RNA1 C
ATOM	2691	N1	C C1105	10.448	-3.539	10.827	1.00	31.92	RNA1 N
ATOM	2692	C2	C C1105	10.029	-4.832	10.461	1.00	29.04	RNA1 C









ATOM	2828	O5*	G D1054	-0.993	13.484	-58.088	1.00	55.82	RNA2 O
ATOM	2829	C5*	G D1054	-2.203	13.659	-58.842	1.00	63.34	RNA2 C
ATOM	2830	C4*	G D1054	-2.607	12.376	-59.540	1.00	61.66	RNA2 C
ATOM	2831	O4*	G D1054	-1.612	11.993	-60.529	1.00	57.48	RNA2 O
ATOM	2832	C3*	G D1054	-2.785	11.116	-58.707	1.00	58.52	RNA2 C
ATOM	2833	O3*	G D1054	-4.027	11.063	-58.021	1.00	50.20	RNA2 O
ATOM	2834	C2*	G D1054	-2.702	10.021	-59.766	1.00	54.72	RNA2 C
ATOM	2835	O2*	G D1054	-3.915	9.849	-60.469	1.00	57.84	RNA2 O
ATOM	2836	C1*	G D1054	-1.657	10.588	-60.723	1.00	42.15	RNA2 C
ATOM	2837	N9	G D1054	-0.347	10.004	-60.453	1.00	43.98	RNA2 N
ATOM	2838	C8	G D1054	0.686	10.525	-59.707	1.00	48.29	RNA2 C
ATOM	2839	N7	G D1054	1.715	9.721	-59.624	1.00	48.90	RNA2 N
ATOM	2840	C5	G D1054	1.340	8.607	-60.367	1.00	43.87	RNA2 C
ATOM	2841	C6	G D1054	2.037	7.396	-60.634	1.00	37.83	RNA2 C
ATOM	2842	O6	G D1054	3.167	7.050	-60.252	1.00	35.95	RNA2 O
ATOM	2843	N1	G D1054	1.279	6.539	-61.428	1.00	42.56	RNA2 N
ATOM	2844	C2	G D1054	0.013	6.807	-61.901	1.00	45.28	RNA2 C
ATOM	2845	N2	G D1054	-0.567	5.854	-62.647	1.00	42.14	RNA2 N
ATOM	2846	N3	G D1054	-0.642	7.925	-61.659	1.00	40.97	RNA2 N
ATOM	2847	C4	G D1054	0.074	8.774	-60.892	1.00	45.06	RNA2 C
ATOM	2848	P	G D1055	-4.174	10.115	-56.729	1.00	60.11	RNA2 P
ATOM	2849	O1P	G D1055	-3.012	10.347	-55.817	1.00	52.31	RNA2 O
ATOM	2850	O2P	G D1055	-5.562	10.287	-56.226	1.00	45.31	RNA2 O
ATOM	2851	O5*	G D1055	-4.016	8.633	-57.297	1.00	61.25	RNA2 O
ATOM	2852	C5*	G D1055	-5.060	8.044	-58.084	1.00	49.39	RNA2 C
ATOM	2853	C4*	G D1055	-4.631	6.705	-58.643	1.00	46.06	RNA2 C
ATOM	2854	O4*	G D1055	-3.395	6.848	-59.392	1.00	46.04	RNA2 O
ATOM	2855	C3*	G D1055	-4.322	5.571	-57.678	1.00	46.58	RNA2 C
ATOM	2856	O3*	G D1055	-5.478	4.904	-57.197	1.00	44.61	RNA2 O
ATOM	2857	C2*	G D1055	-3.512	4.627	-58.556	1.00	50.61	RNA2 C
ATOM	2858	O2*	G D1055	-4.337	3.844	-59.397	1.00	57.17	RNA2 O
ATOM	2859	C1*	G D1055	-2.719	5.604	-59.419	1.00	37.93	RNA2 C
ATOM	2860	N9	G D1055	-1.364	5.764	-58.905	1.00	28.75	RNA2 N
ATOM	2861	C8	G D1055	-0.813	6.849	-58.266	1.00	28.74	RNA2 C
ATOM	2862	N7	G D1055	0.437	6.662	-57.928	1.00	31.82	RNA2 N
ATOM	2863	C5	G D1055	0.725	5.377	-58.371	1.00	24.53	RNA2 C
ATOM	2864	C6	G D1055	1.924	4.619	-58.293	1.00	28.90	RNA2 C
ATOM	2865	O6	G D1055	3.010	4.943	-57.807	1.00	32.85	RNA2 O
ATOM	2866	N1	G D1055	1.771	3.360	-58.862	1.00	26.15	RNA2 N
ATOM	2867	C2	G D1055	0.615	2.884	-59.432	1.00	32.58	RNA2 C
ATOM	2868	N2	G D1055	0.658	1.635	-59.922	1.00	28.69	RNA2 N
ATOM	2869	N3	G D1055	-0.505	3.580	-59.514	1.00	26.67	RNA2 N
ATOM	2870	C4	G D1055	-0.377	4.809	-58.971	1.00	28.85	RNA2 C
ATOM	2871	P	G D1056	-5.427	4.178	-55.764	1.00	41.37	RNA2 P
ATOM	2872	O1P	G D1056	-5.088	5.212	-54.752	1.00	49.91	RNA2 O

ATOM	2873	O2P	G D1056	-6.660	3.370	-55.603	1.00	41.24	RNA2 O
ATOM	2874	O5*	G D1056	-4.173	3.205	-55.857	1.00	31.72	RNA2 O
ATOM	2875	C5*	G D1056	-4.288	1.915	-56.458	1.00	26.06	RNA2 C
ATOM	2876	C4*	G D1056	-2.992	1.163	-56.310	1.00	30.23	RNA2 C
ATOM	2877	O4*	G D1056	-1.926	1.929	-56.923	1.00	33.12	RNA2 O
ATOM	2878	C3*	G D1056	-2.520	0.944	-54.886	1.00	25.25	RNA2 C
ATOM	2879	O3*	G D1056	-3.091	-0.214	-54.323	1.00	32.82	RNA2 O
ATOM	2880	C2*	G D1056	-1.015	0.792	-55.044	1.00	30.19	RNA2 C
ATOM	2881	O2*	G D1056	-0.631	-0.515	-55.418	1.00	28.72	RNA2 O
ATOM	2882	C1*	G D1056	-0.728	1.769	-56.181	1.00	29.85	RNA2 C
ATOM	2883	N9	G D1056	-0.326	3.081	-55.682	1.00	33.20	RNA2 N
ATOM	2884	C8	G D1056	-1.142	4.165	-55.453	1.00	31.51	RNA2 C
ATOM	2885	N7	G D1056	-0.496	5.205	-55.003	1.00	40.50	RNA2 N
ATOM	2886	C5	G D1056	0.825	4.784	-54.926	1.00	37.25	RNA2 C
ATOM	2887	C6	G D1056	1.985	5.481	-54.505	1.00	45.50	RNA2 C
ATOM	2888	O6	G D1056	2.078	6.654	-54.106	1.00	54.00	RNA2 O
ATOM	2889	N1	G D1056	3.122	4.677	-54.584	1.00	42.27	RNA2 N
ATOM	2890	C2	G D1056	3.138	3.372	-55.020	1.00	38.28	RNA2 C
ATOM	2891	N2	G D1056	4.337	2.765	-55.040	1.00	33.41	RNA2 N
ATOM	2892	N3	G D1056	2.060	2.712	-55.413	1.00	35.91	RNA2 N
ATOM	2893	C4	G D1056	0.947	3.474	-55.341	1.00	31.74	RNA2 C
ATOM	2894	P	A D1057	-3.445	-0.241	-52.765	1.00	34.80	RNA2 P
ATOM	2895	O1P	A D1057	-2.899	-1.503	-52.213	1.00	40.31	RNA2 O
ATOM	2896	O2P	A D1057	-3.058	1.055	-52.152	1.00	39.35	RNA2 O
ATOM	2897	O5*	A D1057	-5.027	-0.331	-52.754	1.00	19.58	RNA2 O
ATOM	2898	C5*	A D1057	-5.823	0.724	-53.304	1.00	24.68	RNA2 C
ATOM	2899	C4*	A D1057	-6.915	0.144	-54.161	1.00	26.68	RNA2 C
ATOM	2900	O4*	A D1057	-6.359	-0.301	-55.425	1.00	40.11	RNA2 O
ATOM	2901	C3*	A D1057	-7.560	-1.100	-53.585	1.00	30.27	RNA2 C
ATOM	2902	O3*	A D1057	-8.559	-0.816	-52.635	1.00	35.52	RNA2 O
ATOM	2903	C2*	A D1057	-8.090	-1.811	-54.820	1.00	30.75	RNA2 C
ATOM	2904	O2*	A D1057	-9.317	-1.270	-55.268	1.00	24.78	RNA2 O
ATOM	2905	C1*	A D1057	-6.991	-1.506	-55.834	1.00	16.37	RNA2 C
ATOM	2906	N9	A D1057	-5.973	-2.559	-55.883	1.00	21.50	RNA2 N
ATOM	2907	C8	A D1057	-4.626	-2.445	-55.613	1.00	18.28	RNA2 C
ATOM	2908	N7	A D1057	-3.962	-3.566	-55.754	1.00	23.67	RNA2 N
ATOM	2909	C5	A D1057	-4.935	-4.484	-56.140	1.00	21.49	RNA2 C
ATOM	2910	C6	A D1057	-4.872	-5.852	-56.447	1.00	17.73	RNA2 C
ATOM	2911	N6	A D1057	-3.748	-6.569	-56.412	1.00	22.33	RNA2 N
ATOM	2912	N1	A D1057	-6.019	-6.470	-56.797	1.00	29.29	RNA2 N
ATOM	2913	C2	A D1057	-7.150	-5.753	-56.829	1.00	30.01	RNA2 C
ATOM	2914	N3	A D1057	-7.337	-4.465	-56.559	1.00	24.69	RNA2 N
ATOM	2915	C4	A D1057	-6.177	-3.879	-56.219	1.00	18.45	RNA2 C
ATOM	2916	P	U D1058	-8.746	-1.807	-51.399	1.00	30.93	RNA2 P
ATOM	2917	O1P	U D1058	-7.361	-2.213	-50.993	1.00	24.94	RNA2 O

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ATOM	2918	O2P	U D1058	-9.669	-1.203	-50.402	1.00	29.08	RNA2 O
ATOM	2919	O5*	U D1058	-9.464	-3.068	-52.042	1.00	30.31	RNA2 O
ATOM	2920	C5*	U D1058	-10.859	-3.043	-52.331	1.00	28.81	RNA2 C
ATOM	2921	C4*	U D1058	-11.349	-4.440	-52.592	1.00	31.83	RNA2 C
ATOM	2922	O4*	U D1058	-10.668	-4.953	-53.765	1.00	33.24	RNA2 O
ATOM	2923	C3*	U D1058	-11.031	-5.471	-51.520	1.00	33.13	RNA2 C
ATOM	2924	O3*	U D1058	-11.925	-5.479	-50.425	1.00	32.98	RNA2 O
ATOM	2925	C2*	U D1058	-11.084	-6.772	-52.299	1.00	29.12	RNA2 C
ATOM	2926	O2*	U D1058	-12.414	-7.204	-52.513	1.00	29.74	RNA2 O
ATOM	2927	C1*	U D1058	-10.455	-6.348	-53.622	1.00	26.32	RNA2 C
ATOM	2928	N1	U D1058	-9.008	-6.614	-53.638	1.00	21.34	RNA2 N
ATOM	2929	C2	U D1058	-8.608	-7.932	-53.803	1.00	24.87	RNA2 C
ATOM	2930	O2	U D1058	-9.402	-8.853	-53.938	1.00	31.94	RNA2 O
ATOM	2931	N3	U D1058	-7.253	-8.136	-53.799	1.00	8.92	RNA2 N
ATOM	2932	C4	U D1058	-6.273	-7.188	-53.647	1.00	22.44	RNA2 C
ATOM	2933	O4	U D1058	-5.088	-7.533	-53.685	1.00	18.08	RNA2 O
ATOM	2934	C5	U D1058	-6.759	-5.848	-53.482	1.00	22.73	RNA2 C
ATOM	2935	C6	U D1058	-8.080	-5.614	-53.488	1.00	18.95	RNA2 C
ATOM	2936	P	G D1059	-11.432	-6.089	-49.022	1.00	29.43	RNA2 P
ATOM	2937	O1P	G D1059	-9.995	-5.757	-48.812	1.00	18.78	RNA2 O
ATOM	2938	O2P	G D1059	-12.431	-5.724	-47.993	1.00	38.92	RNA2 O
ATOM	2939	O5*	G D1059	-11.490	-7.659	-49.247	1.00	34.42	RNA2 O
ATOM	2940	C5*	G D1059	-12.729	-8.312	-49.534	1.00	29.33	RNA2 C
ATOM	2941	C4*	G D1059	-12.525	-9.801	-49.573	1.00	27.67	RNA2 C
ATOM	2942	O4*	G D1059	-11.608	-10.126	-50.645	1.00	28.30	RNA2 O
ATOM	2943	C3*	G D1059	-11.883	-10.411	-48.339	1.00	32.02	RNA2 C
ATOM	2944	O3*	G D1059	-12.840	-10.666	-47.314	1.00	37.54	RNA2 O
ATOM	2945	C2*	G D1059	-11.260	-11.691	-48.887	1.00	27.34	RNA2 C
ATOM	2946	O2*	G D1059	-12.207	-12.736	-48.993	1.00	21.26	RNA2 O
ATOM	2947	C1*	G D1059	-10.838	-11.258	-50.289	1.00	18.26	RNA2 C
ATOM	2948	N9	G D1059	-9.425	-10.920	-50.414	1.00	11.76	RNA2 N
ATOM	2949	C8	G D1059	-8.846	-9.686	-50.262	1.00	10.37	RNA2 C
ATOM	2950	N7	G D1059	-7.552	-9.700	-50.455	1.00	15.12	RNA2 N
ATOM	2951	C5	G D1059	-7.260	-11.026	-50.747	1.00	5.51	RNA2 C
ATOM	2952	C6	G D1059	-6.022	-11.652	-51.055	1.00	15.78	RNA2 C
ATOM	2953	O6	G D1059	-4.892	-11.145	-51.124	1.00	17.40	RNA2 O
ATOM	2954	N1	G D1059	-6.184	-13.009	-51.300	1.00	12.54	RNA2 N
ATOM	2955	C2	G D1059	-7.377	-13.685	-51.256	1.00	23.87	RNA2 C
ATOM	2956	N2	G D1059	-7.326	-14.997	-51.540	1.00	21.07	RNA2 N
ATOM	2957	N3	G D1059	-8.536	-13.119	-50.962	1.00	20.56	RNA2 N
ATOM	2958	C4	G D1059	-8.404	-11.794	-50.723	1.00	17.53	RNA2 C
ATOM	2959	P	U D1060	-12.363	-10.713	-45.780	1.00	31.30	RNA2 P
ATOM	2960	O1P	U D1060	-13.473	-10.167	-44.963	1.00	29.83	RNA2 O
ATOM	2961	O2P	U D1060	-11.840	-12.074	-45.484	1.00	37.29	RNA2 O
ATOM	2962	O5*	U D1060	-11.129	-9.708	-45.745	1.00	25.29	RNA2 O

ATOM	2963	C5*	U D1060	-10.735	-9.064	-44.527	1.00	22.54	RNA2 C
ATOM	2964	C4*	U D1060	-9.378	-8.435	-44.692	1.00	22.65	RNA2 C
ATOM	2965	O4*	U D1060	-8.401	-9.481	-44.882	1.00	24.56	RNA2 O
ATOM	2966	C3*	U D1060	-9.238	-7.481	-45.870	1.00	26.03	RNA2 C
ATOM	2967	O3*	U D1060	-8.303	-6.454	-45.522	1.00	41.53	RNA2 O
ATOM	2968	C2*	U D1060	-8.608	-8.361	-46.946	1.00	31.11	RNA2 C
ATOM	2969	O2*	U D1060	-7.808	-7.616	-47.841	1.00	45.38	RNA2 O
ATOM	2970	C1*	U D1060	-7.735	-9.299	-46.110	1.00	26.61	RNA2 C
ATOM	2971	N1	U D1060	-7.519	-10.632	-46.690	1.00	21.85	RNA2 N
ATOM	2972	C2	U D1060	-6.291	-10.898	-47.261	1.00	23.55	RNA2 C
ATOM	2973	O2	U D1060	-5.402	-10.063	-47.355	1.00	21.48	RNA2 O
ATOM	2974	N3	U D1060	-6.141	-12.182	-47.726	1.00	25.97	RNA2 N
ATOM	2975	C4	U D1060	-7.076	-13.199	-47.691	1.00	28.32	RNA2 C
ATOM	2976	O4	U D1060	-6.778	-14.311	-48.139	1.00	27.53	RNA2 O
ATOM	2977	C5	U D1060	-8.329	-12.837	-47.107	1.00	18.41	RNA2 C
ATOM	2978	C6	U D1060	-8.507	-11.600	-46.642	1.00	21.87	RNA2 C
ATOM	2979	P	U D1061	-8.630	-5.419	-44.325	1.00	28.91	RNA2 P
ATOM	2980	O1P	U D1061	-8.173	-4.091	-44.810	1.00	33.68	RNA2 O
ATOM	2981	O2P	U D1061	-10.037	-5.590	-43.863	1.00	15.62	RNA2 O
ATOM	2982	O5*	U D1061	-7.649	-5.888	-43.161	1.00	19.70	RNA2 O
ATOM	2983	C5*	U D1061	-6.225	-5.745	-43.301	1.00	18.21	RNA2 C
ATOM	2984	C4*	U D1061	-5.514	-6.526	-42.225	1.00	27.99	RNA2 C
ATOM	2985	O4*	U D1061	-5.894	-5.996	-40.927	1.00	36.85	RNA2 O
ATOM	2986	C3*	U D1061	-5.800	-8.028	-42.181	1.00	29.80	RNA2 C
ATOM	2987	O3*	U D1061	-4.608	-8.696	-41.772	1.00	33.59	RNA2 O
ATOM	2988	C2*	U D1061	-6.812	-8.151	-41.043	1.00	33.22	RNA2 C
ATOM	2989	O2*	U D1061	-6.748	-9.417	-40.415	1.00	27.78	RNA2 O
ATOM	2990	C1*	U D1061	-6.313	-7.055	-40.102	1.00	42.74	RNA2 C
ATOM	2991	N1	U D1061	-7.205	-6.543	-39.046	1.00	44.96	RNA2 N
ATOM	2992	C2	U D1061	-6.737	-6.649	-37.742	1.00	53.51	RNA2 C
ATOM	2993	O2	U D1061	-5.650	-7.143	-37.464	1.00	44.65	RNA2 O
ATOM	2994	N3	U D1061	-7.579	-6.157	-36.776	1.00	60.76	RNA2 N
ATOM	2995	C4	U D1061	-8.811	-5.585	-36.961	1.00	51.80	RNA2 C
ATOM	2996	O4	U D1061	-9.435	-5.195	-35.977	1.00	48.61	RNA2 O
ATOM	2997	C5	U D1061	-9.240	-5.508	-38.333	1.00	40.80	RNA2 C
ATOM	2998	C6	U D1061	-8.440	-5.979	-39.307	1.00	43.37	RNA2 C
ATOM	2999	P	G D1062	-3.700	-9.466	-42.848	1.00	33.56	RNA2 P
ATOM	3000	O1P	G D1062	-3.835	-8.777	-44.158	1.00	35.31	RNA2 O
ATOM	3001	O2P	G D1062	-2.353	-9.644	-42.252	1.00	21.04	RNA2 O
ATOM	3002	O5*	G D1062	-4.367	-10.905	-42.956	1.00	30.74	RNA2 O
ATOM	3003	C5*	G D1062	-5.563	-11.128	-43.737	1.00	36.95	RNA2 C
ATOM	3004	C4*	G D1062	-5.583	-12.554	-44.235	1.00	30.45	RNA2 C
ATOM	3005	O4*	G D1062	-4.531	-12.739	-45.222	1.00	26.47	RNA2 O
ATOM	3006	C3*	G D1062	-5.264	-13.550	-43.139	1.00	20.89	RNA2 C
ATOM	3007	O3*	G D1062	-6.428	-13.905	-42.431	1.00	31.67	RNA2 O

ATOM	3008	C2*	G D1062	-4.625	-14.707	-43.894	1.00	23.56	RNA2 C
ATOM	3009	O2*	G D1062	-5.589	-15.567	-44.466	1.00	18.76	RNA2 O
ATOM	3010	C1*	G D1062	-3.854	-13.963	-44.988	1.00	16.90	RNA2 C
ATOM	3011	N9	G D1062	-2.473	-13.642	-44.620	1.00	13.03	RNA2 N
ATOM	3012	C8	G D1062	-1.919	-12.387	-44.523	1.00	19.49	RNA2 C
ATOM	3013	N7	G D1062	-0.660	-12.404	-44.173	1.00	13.70	RNA2 N
ATOM	3014	C5	G D1062	-0.362	-13.749	-44.024	1.00	14.04	RNA2 C
ATOM	3015	C6	G D1062	0.850	-14.379	-43.651	1.00	24.18	RNA2 C
ATOM	3016	O6	G D1062	1.933	-13.852	-43.356	1.00	29.04	RNA2 O
ATOM	3017	N1	G D1062	0.723	-15.765	-43.634	1.00	22.87	RNA2 N
ATOM	3018	C2	G D1062	-0.427	-16.456	-43.927	1.00	30.15	RNA2 C
ATOM	3019	N2	G D1062	-0.349	-17.795	-43.849	1.00	24.93	RNA2 N
ATOM	3020	N3	G D1062	-1.570	-15.878	-44.269	1.00	30.88	RNA2 N
ATOM	3021	C4	G D1062	-1.466	-14.531	-44.300	1.00	16.88	RNA2 C
ATOM	3022	P	G D1063	-6.322	-14.242	-40.874	1.00	28.41	RNA2 P
ATOM	3023	O1P	G D1063	-5.463	-13.199	-40.266	1.00	27.32	RNA2 O
ATOM	3024	O2P	G D1063	-7.701	-14.468	-40.367	1.00	29.73	RNA2 O
ATOM	3025	O5*	G D1063	-5.523	-15.617	-40.821	1.00	30.17	RNA2 O
ATOM	3026	C5*	G D1063	-6.184	-16.864	-41.087	1.00	24.95	RNA2 C
ATOM	3027	C4*	G D1063	-5.241	-18.011	-40.832	1.00	20.87	RNA2 C
ATOM	3028	O4*	G D1063	-4.075	-17.850	-41.677	1.00	27.19	RNA2 O
ATOM	3029	C3*	G D1063	-4.659	-18.092	-39.434	1.00	26.89	RNA2 C
ATOM	3030	O3*	G D1063	-5.539	-18.706	-38.508	1.00	40.50	RNA2 O
ATOM	3031	C2*	G D1063	-3.373	-18.869	-39.659	1.00	23.40	RNA2 C
ATOM	3032	O2*	G D1063	-3.601	-20.256	-39.810	1.00	29.18	RNA2 O
ATOM	3033	C1*	G D1063	-2.919	-18.297	-40.994	1.00	21.30	RNA2 C
ATOM	3034	N9	G D1063	-2.022	-17.158	-40.820	1.00	18.48	RNA2 N
ATOM	3035	C8	G D1063	-2.309	-15.827	-41.016	1.00	13.94	RNA2 C
ATOM	3036	N7	G D1063	-1.283	-15.044	-40.798	1.00	19.66	RNA2 N
ATOM	3037	C5	G D1063	-0.260	-15.909	-40.428	1.00	17.05	RNA2 C
ATOM	3038	C6	G D1063	1.093	-15.646	-40.066	1.00	24.81	RNA2 C
ATOM	3039	O6	G D1063	1.680	-14.559	-39.999	1.00	27.63	RNA2 O
ATOM	3040	N1	G D1063	1.776	-16.819	-39.756	1.00	29.06	RNA2 N
ATOM	3041	C2	G D1063	1.234	-18.080	-39.781	1.00	24.76	RNA2 C
ATOM	3042	N2	G D1063	2.051	-19.081	-39.433	1.00	26.32	RNA2 N
ATOM	3043	N3	G D1063	-0.018	-18.340	-40.119	1.00	25.89	RNA2 N
ATOM	3044	C4	G D1063	-0.702	-17.217	-40.429	1.00	24.85	RNA2 C
ATOM	3045	P	C D1064	-5.606	-18.145	-37.003	1.00	33.12	RNA2 P
ATOM	3046	O1P	C D1064	-5.740	-16.669	-37.090	1.00	33.72	RNA2 O
ATOM	3047	O2P	C D1064	-6.628	-18.934	-36.261	1.00	34.10	RNA2 O
ATOM	3048	O5*	C D1064	-4.159	-18.476	-36.424	1.00	27.13	RNA2 O
ATOM	3049	C5*	C D1064	-3.695	-19.826	-36.395	1.00	16.79	RNA2 C
ATOM	3050	C4*	C D1064	-2.235	-19.884	-36.032	1.00	25.70	RNA2 C
ATOM	3051	O4*	C D1064	-1.436	-19.19				

ATOM	3053	O3*	C D1064	-2.095	-20.085	-33.611	1.00	37.04	RNA2 O
ATOM	3054	C2*	C D1064	-0.315	-19.047	-34.923	1.00	30.06	RNA2 C
ATOM	3055	O2*	C D1064	0.445	-20.216	-34.696	1.00	28.38	RNA2 O
ATOM	3056	C1*	C D1064	-0.251	-18.704	-36.409	1.00	30.33	RNA2 C
ATOM	3057	N1	C D1064	-0.140	-17.251	-36.627	1.00	20.71	RNA2 N
ATOM	3058	C2	C D1064	1.114	-16.655	-36.474	1.00	24.44	RNA2 C
ATOM	3059	O2	C D1064	2.086	-17.365	-36.175	1.00	30.49	RNA2 O
ATOM	3060	N3	C D1064	1.237	-15.325	-36.654	1.00	26.69	RNA2 N
ATOM	3061	C4	C D1064	0.170	-14.591	-36.976	1.00	20.50	RNA2 C
ATOM	3062	N4	C D1064	0.347	-13.279	-37.141	1.00	22.60	RNA2 N
ATOM	3063	C5	C D1064	-1.120	-15.169	-37.143	1.00	10.11	RNA2 C
ATOM	3064	C6	C D1064	-1.229	-16.492	-36.962	1.00	23.85	RNA2 C
ATOM	3065	P	U D1065	-2.513	-19.420	-32.214	1.00	35.56	RNA2 P
ATOM	3066	O1P	U D1065	-3.615	-18.460	-32.467	1.00	26.06	RNA2 O
ATOM	3067	O2P	U D1065	-2.716	-20.527	-31.248	1.00	43.50	RNA2 O
ATOM	3068	O5*	U D1065	-1.209	-18.600	-31.807	1.00	27.70	RNA2 O
ATOM	3069	C5*	U D1065	0.044	-19.282	-31.609	1.00	30.92	RNA2 C
ATOM	3070	C4*	U D1065	1.168	-18.287	-31.469	1.00	30.67	RNA2 C
ATOM	3071	O4*	U D1065	1.332	-17.559	-32.713	1.00	39.57	RNA2 O
ATOM	3072	C3*	U D1065	0.951	-17.209	-30.423	1.00	36.18	RNA2 C
ATOM	3073	O3*	U D1065	1.285	-17.667	-29.123	1.00	36.24	RNA2 O
ATOM	3074	C2*	U D1065	1.843	-16.076	-30.921	1.00	38.21	RNA2 C
ATOM	3075	O2*	U D1065	3.207	-16.224	-30.578	1.00	34.14	RNA2 O
ATOM	3076	C1*	U D1065	1.692	-16.216	-32.437	1.00	34.96	RNA2 C
ATOM	3077	N1	U D1065	0.645	-15.327	-32.968	1.00	22.93	RNA2 N
ATOM	3078	C2	U D1065	1.028	-14.066	-33.377	1.00	24.04	RNA2 C
ATOM	3079	O2	U D1065	2.187	-13.674	-33.325	1.00	20.47	RNA2 O
ATOM	3080	N3	U D1065	0.008	-13.276	-33.849	1.00	17.91	RNA2 N
ATOM	3081	C4	U D1065	-1.325	-13.612	-33.954	1.00	25.02	RNA2 C
ATOM	3082	O4	U D1065	-2.125	-12.793	-34.424	1.00	30.88	RNA2 O
ATOM	3083	C5	U D1065	-1.640	-14.934	-33.511	1.00	26.71	RNA2 C
ATOM	3084	C6	U D1065	-0.670	-15.727	-33.046	1.00	28.23	RNA2 C
ATOM	3085	P	U D1066	0.342	-17.279	-27.876	1.00	35.54	RNA2 P
ATOM	3086	O1P	U D1066	-1.089	-17.498	-28.212	1.00	19.51	RNA2 O
ATOM	3087	O2P	U D1066	0.927	-17.960	-26.692	1.00	43.24	RNA2 O
ATOM	3088	O5*	U D1066	0.552	-15.708	-27.728	1.00	32.79	RNA2 O
ATOM	3089	C5*	U D1066	1.867	-15.163	-27.509	1.00	39.57	RNA2 C
ATOM	3090	C4*	U D1066	1.853	-13.664	-27.695	1.00	41.26	RNA2 C
ATOM	3091	O4*	U D1066	1.606	-13.339	-29.088	1.00	50.01	RNA2 O
ATOM	3092	C3*	U D1066	0.773	-12.909	-26.935	1.00	46.81	RNA2 C
ATOM	3093	O3*	U D1066	1.137	-12.653	-25.587	1.00	47.16	RNA2 O
ATOM	3094	C2*	U D1066	0.645	-11.626	-27.743	1.00	45.38	RNA2 C
ATOM	3095	O2*	U D1066	1.671	-10.702	-27.422	1.00	47.24	RNA2 O
ATOM	3096	C1*	U D1066	0.848	-12.142	-29.168	1.00	44.66	RNA2 C
ATOM	3097	N1	U D1066	-0.437	-12.423	-29.835	1.00	36.02	RNA2 N

ATOM	3098	C2	U D1066	-1.001	-11.401	-30.583	1.00	31.01	RNA2 C
ATOM	3099	O2	U D1066	-0.450	-10.325	-30.752	1.00	24.12	RNA2 O
ATOM	3100	N3	U D1066	-2.231	-11.687	-31.131	1.00	26.04	RNA2 N
ATOM	3101	C4	U D1066	-2.939	-12.872	-31.028	1.00	32.10	RNA2 C
ATOM	3102	O4	U D1066	-4.082	-12.941	-31.501	1.00	32.26	RNA2 O
ATOM	3103	C5	U D1066	-2.276	-13.895	-30.271	1.00	27.27	RNA2 C
ATOM	3104	C6	U D1066	-1.080	-13.644	-29.712	1.00	35.51	RNA2 C
ATOM	3105	P	A D1067	0.011	-12.695	-24.442	1.00	41.56	RNA2 P
ATOM	3106	O1P	A D1067	-0.869	-13.868	-24.667	1.00	35.90	RNA2 O
ATOM	3107	O2P	A D1067	0.710	-12.532	-23.138	1.00	61.37	RNA2 O
ATOM	3108	O5*	A D1067	-0.877	-11.403	-24.702	1.00	37.80	RNA2 O
ATOM	3109	C5*	A D1067	-2.175	-11.275	-24.099	1.00	33.78	RNA2 C
ATOM	3110	C4*	A D1067	-2.689	-9.870	-24.284	1.00	40.27	RNA2 C
ATOM	3111	O4*	A D1067	-1.791	-8.952	-23.617	1.00	40.68	RNA2 O
ATOM	3112	C3*	A D1067	-2.714	-9.402	-25.727	1.00	40.11	RNA2 C
ATOM	3113	O3*	A D1067	-3.918	-9.794	-26.362	1.00	46.79	RNA2 O
ATOM	3114	C2*	A D1067	-2.560	-7.892	-25.606	1.00	33.18	RNA2 C
ATOM	3115	O2*	A D1067	-3.785	-7.245	-25.315	1.00	34.55	RNA2 O
ATOM	3116	C1*	A D1067	-1.637	-7.782	-24.394	1.00	30.38	RNA2 C
ATOM	3117	N9	A D1067	-0.216	-7.636	-24.699	1.00	18.52	RNA2 N
ATOM	3118	C8	A D1067	0.791	-8.539	-24.462	1.00	19.03	RNA2 C
ATOM	3119	N7	A D1067	1.987	-8.090	-24.769	1.00	23.17	RNA2 N
ATOM	3120	C5	A D1067	1.748	-6.814	-25.262	1.00	12.64	RNA2 C
ATOM	3121	C6	A D1067	2.605	-5.811	-25.748	1.00	16.33	RNA2 C
ATOM	3122	N6	A D1067	3.934	-5.945	-25.831	1.00	21.10	RNA2 N
ATOM	3123	N1	A D1067	2.046	-4.651	-26.154	1.00	17.93	RNA2 N
ATOM	3124	C2	A D1067	0.714	-4.518	-26.077	1.00	24.51	RNA2 C
ATOM	3125	N3	A D1067	-0.197	-5.388	-25.642	1.00	23.41	RNA2 N
ATOM	3126	C4	A D1067	0.393	-6.528	-25.240	1.00	22.32	RNA2 C
ATOM	3127	P	G D1068	-3.863	-10.352	-27.861	1.00	37.45	RNA2 P
ATOM	3128	O1P	G D1068	-2.775	-11.365	-27.915	1.00	32.87	RNA2 O
ATOM	3129	O2P	G D1068	-5.247	-10.719	-28.265	1.00	30.61	RNA2 O
ATOM	3130	O5*	G D1068	-3.399	-9.084	-28.697	1.00	34.59	RNA2 O
ATOM	3131	C5*	G D1068	-4.254	-7.938	-28.794	1.00	32.91	RNA2 C
ATOM	3132	C4*	G D1068	-3.550	-6.828	-29.521	1.00	39.65	RNA2 C
ATOM	3133	O4*	G D1068	-2.460	-6.334	-28.708	1.00	34.36	RNA2 O
ATOM	3134	C3*	G D1068	-2.908	-7.218	-30.840	1.00	41.96	RNA2 C
ATOM	3135	O3*	G D1068	-3.874	-7.194	-31.893	1.00	38.73	RNA2 O
ATOM	3136	C2*	G D1068	-1.811	-6.168	-30.989	1.00	37.55	RNA2 C
ATOM	3137	O2*	G D1068	-2.315	-4.944	-31.487	1.00	54.39	RNA2 O
ATOM	3138	C1*	G D1068	-1.382	-5.951	-29.535	1.00	22.83	RNA2 C
ATOM	3139	N9	G D1068	-0.226	-6.739	-29.134	1.00	20.42	RNA2 N
ATOM	3140	C8	G D1068	-0.246	-8.011	-28.616	1.00	22.08	RNA2 C
ATOM	3141	N7	G D1068	0.944	-8.464	-28.328	1.00	22.50	RNA2 N
ATOM	3142	C5	G D1068	1.803	-7.433	-28.683	1.00	10.90	RNA2 C

ATOM	3143	C6	G D1068	3.211	-7.347	-28.595	1.00	18.64	RNA2 C
ATOM	3144	O6	G D1068	4.011	-8.196	-28.176	1.00	32.91	RNA2 O
ATOM	3145	N1	G D1068	3.679	-6.123	-29.060	1.00	12.16	RNA2 N
ATOM	3146	C2	G D1068	2.894	-5.115	-29.547	1.00	13.74	RNA2 C
ATOM	3147	N2	G D1068	3.543	-4.013	-29.960	1.00	20.53	RNA2 N
ATOM	3148	N3	G D1068	1.575	-5.179	-29.629	1.00	16.63	RNA2 N
ATOM	3149	C4	G D1068	1.100	-6.360	-29.184	1.00	16.14	RNA2 C
ATOM	3150	P	A D1069	-3.995	-8.447	-32.902	1.00	27.21	RNA2 P
ATOM	3151	O1P	A D1069	-4.082	-9.718	-32.124	1.00	34.28	RNA2 O
ATOM	3152	O2P	A D1069	-5.070	-8.102	-33.864	1.00	29.02	RNA2 O
ATOM	3153	O5*	A D1069	-2.601	-8.445	-33.661	1.00	13.61	RNA2 O
ATOM	3154	C5*	A D1069	-2.231	-7.337	-34.472	1.00	12.04	RNA2 C
ATOM	3155	C4*	A D1069	-0.867	-7.557	-35.055	1.00	21.87	RNA2 C
ATOM	3156	O4*	A D1069	0.149	-7.322	-34.046	1.00	32.63	RNA2 O
ATOM	3157	C3*	A D1069	-0.590	-8.954	-35.628	1.00	35.90	RNA2 C
ATOM	3158	O3*	A D1069	0.162	-8.819	-36.833	1.00	43.63	RNA2 O
ATOM	3159	C2*	A D1069	0.352	-9.560	-34.592	1.00	35.57	RNA2 C
ATOM	3160	O2*	A D1069	1.241	-10.526	-35.127	1.00	44.23	RNA2 O
ATOM	3161	C1*	A D1069	1.127	-8.311	-34.199	1.00	42.00	RNA2 C
ATOM	3162	N9	A D1069	2.031	-8.358	-33.054	1.00	38.32	RNA2 N
ATOM	3163	C8	A D1069	2.071	-9.207	-31.976	1.00	30.76	RNA2 C
ATOM	3164	N7	A D1069	3.141	-9.059	-31.233	1.00	35.91	RNA2 N
ATOM	3165	C5	A D1069	3.827	-8.017	-31.841	1.00	33.30	RNA2 C
ATOM	3166	C6	A D1069	5.053	-7.392	-31.552	1.00	39.74	RNA2 C
ATOM	3167	N6	A D1069	5.850	-7.751	-30.540	1.00	50.68	RNA2 N
ATOM	3168	N1	A D1069	5.443	-6.375	-32.353	1.00	41.06	RNA2 N
ATOM	3169	C2	A D1069	4.649	-6.022	-33.371	1.00	43.25	RNA2 C
ATOM	3170	N3	A D1069	3.483	-6.540	-33.747	1.00	36.03	RNA2 N
ATOM	3171	C4	A D1069	3.131	-7.548	-32.935	1.00	31.57	RNA2 C
ATOM	3172	P	A D1070	-0.353	-9.514	-38.183	1.00	39.29	RNA2 P
ATOM	3173	O1P	A D1070	0.847	-9.589	-39.057	1.00	23.58	RNA2 O
ATOM	3174	O2P	A D1070	-1.128	-10.747	-37.873	1.00	27.46	RNA2 O
ATOM	3175	O5*	A D1070	-1.376	-8.452	-38.783	1.00	32.87	RNA2 O
ATOM	3176	C5*	A D1070	-0.906	-7.233	-39.388	1.00	32.49	RNA2 C
ATOM	3177	C4*	A D1070	-2.018	-6.594	-40.179	1.00	35.94	RNA2 C
ATOM	3178	O4*	A D1070	-3.134	-6.304	-39.296	1.00	34.73	RNA2 O
ATOM	3179	C3*	A D1070	-1.665	-5.292	-40.885	1.00	39.27	RNA2 C
ATOM	3180	O3*	A D1070	-2.329	-5.275	-42.147	1.00	42.75	RNA2 O
ATOM	3181	C2*	A D1070	-2.248	-4.225	-39.960	1.00	39.48	RNA2 C
ATOM	3182	O2*	A D1070	-2.656	-3.052	-40.635	1.00	46.91	RNA2 O
ATOM	3183	C1*	A D1070	-3.468	-4.935	-39.379	1.00	38.47	RNA2 C
ATOM	3184	N9	A D1070	-3.821	-4.467	-38.038	1.00	42.60	RNA2 N
ATOM	3185	C8	A D1070	-3.112	-4.646	-36.878	1.00	43.81	RNA2 C
ATOM	3186	N7	A D1070	-3.690	-4.133	-35.822	1.00	45.93	RNA2 N
ATOM	3187	C5	A D1070	-4.854	-3.570	-36.318	1.00	44.50	RNA2 C



ATOM	3188	C6	A D1070	-5.898	-2.873	-35.697	1.00	50.91	RNA2 C
ATOM	3189	N6	A D1070	-5.936	-2.617	-34.390	1.00	62.29	RNA2 N
ATOM	3190	N1	A D1070	-6.915	-2.441	-36.474	1.00	49.05	RNA2 N
ATOM	3191	C2	A D1070	-6.870	-2.698	-37.783	1.00	37.67	RNA2 C
ATOM	3192	N3	A D1070	-5.940	-3.344	-38.485	1.00	40.26	RNA2 N
ATOM	3193	C4	A D1070	-4.946	-3.761	-37.683	1.00	42.22	RNA2 C
ATOM	3194	P	G D1071	-1.684	-4.476	-43.382	1.00	30.55	RNA2 P
ATOM	3195	O1P	G D1071	-2.623	-4.642	-44.520	1.00	33.24	RNA2 O
ATOM	3196	O2P	G D1071	-1.310	-3.114	-42.932	1.00	42.96	RNA2 O
ATOM	3197	O5*	G D1071	-0.331	-5.246	-43.697	1.00	21.65	RNA2 O
ATOM	3198	C5*	G D1071	-0.333	-6.592	-44.214	1.00	29.38	RNA2 C
ATOM	3199	C4*	G D1071	1.026	-6.907	-44.779	1.00	23.80	RNA2 C
ATOM	3200	O4*	G D1071	1.238	-6.061	-45.928	1.00	28.20	RNA2 O
ATOM	3201	C3*	G D1071	2.141	-6.557	-43.811	1.00	30.81	RNA2 C
ATOM	3202	O3*	G D1071	2.441	-7.666	-42.979	1.00	41.31	RNA2 O
ATOM	3203	C2*	G D1071	3.288	-6.132	-44.719	1.00	22.22	RNA2 C
ATOM	3204	O2*	G D1071	4.080	-7.199	-45.191	1.00	28.60	RNA2 O
ATOM	3205	C1*	G D1071	2.532	-5.498	-45.883	1.00	21.88	RNA2 C
ATOM	3206	N9	G D1071	2.369	-4.053	-45.773	1.00	20.68	RNA2 N
ATOM	3207	C8	G D1071	1.186	-3.366	-45.636	1.00	17.70	RNA2 C
ATOM	3208	N7	G D1071	1.347	-2.072	-45.623	1.00	24.21	RNA2 N
ATOM	3209	C5	G D1071	2.716	-1.895	-45.742	1.00	13.42	RNA2 C
ATOM	3210	C6	G D1071	3.478	-0.710	-45.794	1.00	24.45	RNA2 C
ATOM	3211	O6	G D1071	3.078	0.460	-45.758	1.00	34.15	RNA2 O
ATOM	3212	N1	G D1071	4.841	-0.981	-45.904	1.00	15.33	RNA2 N
ATOM	3213	C2	G D1071	5.395	-2.241	-45.961	1.00	23.28	RNA2 C
ATOM	3214	N2	G D1071	6.734	-2.306	-46.052	1.00	12.46	RNA2 N
ATOM	3215	N3	G D1071	4.686	-3.356	-45.925	1.00	19.68	RNA2 N
ATOM	3216	C4	G D1071	3.363	-3.109	-45.817	1.00	12.68	RNA2 C
ATOM	3217	P	C D1072	2.695	-7.430	-41.419	1.00	33.36	RNA2 P
ATOM	3218	O1P	C D1072	1.653	-6.490	-40.920	1.00	33.81	RNA2 O
ATOM	3219	O2P	C D1072	2.864	-8.759	-40.777	1.00	35.75	RNA2 O
ATOM	3220	O5*	C D1072	4.090	-6.677	-41.393	1.00	20.85	RNA2 O
ATOM	3221	C5*	C D1072	5.294	-7.370	-41.724	1.00	18.04	RNA2 C
ATOM	3222	C4*	C D1072	6.458	-6.420	-41.676	1.00	27.13	RNA2 C
ATOM	3223	O4*	C D1072	6.309	-5.437	-42.729	1.00	37.39	RNA2 O
ATOM	3224	C3*	C D1072	6.577	-5.591	-40.408	1.00	33.89	RNA2 C
ATOM	3225	O3*	C D1072	7.216	-6.295	-39.352	1.00	27.21	RNA2 O
ATOM	3226	C2*	C D1072	7.364	-4.376	-40.882	1.00	36.24	RNA2 C
ATOM	3227	O2*	C D1072	8.753	-4.637	-40.967	1.00	40.82	RNA2 O
ATOM	3228	C1*	C D1072	6.803	-4.182	-42.291	1.00	32.40	RNA2 C
ATOM	3229	N1	C D1072	5.704	-3.196	-42.347	1.00	21.10	RNA2 N
ATOM	3230	C2	C D1072	6.015	-1.860	-42.594	1.00	22.51	RNA2 C
ATOM	3231	O2	C D1072	7.206	-1.541	-42.755	1.00	32.30	RNA2 O
ATOM	3232	N3	C D1072	5.016	-0.947	-42.647	1.00	18.99	RNA2 N



ATOM	3278	C2	G D1074	4.597 -15.219 -35.379	1.00 34.56	RNA2 C
ATOM	3279	N2	G D1074	4.134 -16.400 -34.936	1.00 34.63	RNA2 N
ATOM	3280	N3	G D1074	5.868 -14.906 -35.205	1.00 31.20	RNA2 N
ATOM	3281	C4	G D1074	6.159 -13.683 -35.695	1.00 23.24	RNA2 C
ATOM	3282	P	C D1075	11.130 -15.471 -38.624	1.00 45.43	RNA2 P
ATOM	3283	O1P	C D1075	10.527 -14.447 -39.520	1.00 54.78	RNA2 O
ATOM	3284	O2P	C D1075	12.430 -16.096 -38.995	1.00 41.18	RNA2 O
ATOM	3285	O5*	C D1075	10.046 -16.607 -38.379	1.00 33.77	RNA2 O
ATOM	3286	C5*	C D1075	10.384 -17.767 -37.609	1.00 31.73	RNA2 C
ATOM	3287	C4*	C D1075	9.233 -18.737 -37.587	1.00 31.50	RNA2 C
ATOM	3288	O4*	C D1075	8.122 -18.137 -36.879	1.00 31.95	RNA2 O
ATOM	3289	C3*	C D1075	8.653 -19.112 -38.940	1.00 34.59	RNA2 C
ATOM	3290	O3*	C D1075	9.390 -20.130 -39.596	1.00 42.98	RNA2 O
ATOM	3291	C2*	C D1075	7.239 -19.539 -38.581	1.00 30.88	RNA2 C
ATOM	3292	O2*	C D1075	7.175 -20.852 -38.064	1.00 24.97	RNA2 O
ATOM	3293	C1*	C D1075	6.902 -18.546 -37.472	1.00 31.01	RNA2 C
ATOM	3294	N1	C D1075	6.223 -17.355 -38.013	1.00 26.90	RNA2 N
ATOM	3295	C2	C D1075	4.831 -17.388 -38.173	1.00 32.07	RNA2 C
ATOM	3296	O2	C D1075	4.206 -18.407 -37.825	1.00 31.32	RNA2 O
ATOM	3297	N3	C D1075	4.204 -16.313 -38.700	1.00 31.52	RNA2 N
ATOM	3298	C4	C D1075	4.908 -15.237 -39.059	1.00 24.70	RNA2 C
ATOM	3299	N4	C D1075	4.246 -14.208 -39.592	1.00 23.21	RNA2 N
ATOM	3300	C5	C D1075	6.320 -15.169 -38.892	1.00 20.78	RNA2 C
ATOM	3301	C6	C D1075	6.932 -16.239 -38.370	1.00 26.55	RNA2 C
ATOM	3302	P	C D1076	9.458 -20.140 -41.200	1.00 41.54	RNA2 P
ATOM	3303	O1P	C D1076	9.719 -18.749 -41.663	1.00 42.90	RNA2 O
ATOM	3304	O2P	C D1076	10.363 -21.241 -41.628	1.00 43.49	RNA2 O
ATOM	3305	O5*	C D1076	7.973 -20.524 -41.614	1.00 36.12	RNA2 O
ATOM	3306	C5*	C D1076	7.448 -21.808 -41.272	1.00 35.93	RNA2 C
ATOM	3307	C4*	C D1076	6.024 -21.941 -41.742	1.00 36.70	RNA2 C
ATOM	3308	O4*	C D1076	5.179 -21.022 -41.003	1.00 41.67	RNA2 O
ATOM	3309	C3*	C D1076	5.735 -21.611 -43.198	1.00 33.47	RNA2 C
ATOM	3310	O3*	C D1076	6.076 -22.654 -44.099	1.00 41.74	RNA2 O
ATOM	3311	C2*	C D1076	4.240 -21.334 -43.160	1.00 38.53	RNA2 C
ATOM	3312	O2*	C D1076	3.483 -22.530 -43.103	1.00 31.60	RNA2 O
ATOM	3313	C1*	C D1076	4.107 -20.590 -41.831	1.00 39.34	RNA2 C
ATOM	3314	N1	C D1076	4.199 -19.124 -42.018	1.00 25.11	RNA2 N
ATOM	3315	C2	C D1076	3.048 -18.421 -42.397	1.00 28.28	RNA2 C
ATOM	3316	O2	C D1076	1.978 -19.045 -42.536	1.00 22.07	RNA2 O
ATOM	3317	N3	C D1076	3.127 -17.083 -42.605	1.00 27.17	RNA2 N
ATOM	3318	C4	C D1076	4.293 -16.452 -42.451	1.00 27.03	RNA2 C
ATOM	3319	N4	C D1076	4.330 -15.136 -42.681	1.00 24.90	RNA2 N
ATOM	3320	C5	C D1076	5.475 -17.140 -42.056	1.00 21.98	RNA2 C
ATOM	3321	C6	C D1076	5.384 -18.460 -41.849	1.00 26.59	RNA2 C
ATOM	3322	P	A D1077	6.603 -22.281 -45.575	1.00 39.40	RNA2 P

ATOM	3323	O1P	A D1077	7.618	-21.198	-45.455	1.00	25.39	RNA2 O
ATOM	3324	O2P	A D1077	6.965	-23.549	-46.255	1.00	45.75	RNA2 O
ATOM	3325	O5*	A D1077	5.308	-21.688	-46.290	1.00	35.32	RNA2 O
ATOM	3326	C5*	A D1077	4.132	-22.496	-46.434	1.00	30.36	RNA2 C
ATOM	3327	C4*	A D1077	2.948	-21.659	-46.863	1.00	39.87	RNA2 C
ATOM	3328	O4*	A D1077	2.657	-20.660	-45.852	1.00	36.52	RNA2 O
ATOM	3329	C3*	A D1077	3.067	-20.856	-48.149	1.00	35.06	RNA2 C
ATOM	3330	O3*	A D1077	2.842	-21.640	-49.313	1.00	33.77	RNA2 O
ATOM	3331	C2*	A D1077	1.981	-19.801	-47.965	1.00	41.16	RNA2 C
ATOM	3332	O2*	A D1077	0.677	-20.271	-48.264	1.00	33.46	RNA2 O
ATOM	3333	C1*	A D1077	2.078	-19.520	-46.466	1.00	37.76	RNA2 C
ATOM	3334	N9	A D1077	2.924	-18.352	-46.211	1.00	25.78	RNA2 N
ATOM	3335	C8	A D1077	4.243	-18.300	-45.836	1.00	18.19	RNA2 C
ATOM	3336	N7	A D1077	4.722	-17.081	-45.756	1.00	17.18	RNA2 N
ATOM	3337	C5	A D1077	3.639	-16.275	-46.087	1.00	18.35	RNA2 C
ATOM	3338	C6	A D1077	3.492	-14.874	-46.208	1.00	24.31	RNA2 C
ATOM	3339	N6	A D1077	4.486	-13.996	-46.008	1.00	25.10	RNA2 N
ATOM	3340	N1	A D1077	2.277	-14.401	-46.558	1.00	22.28	RNA2 N
ATOM	3341	C2	A D1077	1.285	-15.278	-46.776	1.00	17.11	RNA2 C
ATOM	3342	N3	A D1077	1.302	-16.604	-46.702	1.00	22.31	RNA2 N
ATOM	3343	C4	A D1077	2.522	-17.044	-46.352	1.00	17.88	RNA2 C
ATOM	3344	P	U D1078	3.650	-21.306	-50.662	1.00	27.11	RNA2 P
ATOM	3345	O1P	U D1078	5.104	-21.343	-50.374	1.00	20.77	RNA2 O
ATOM	3346	O2P	U D1078	3.091	-22.176	-51.728	1.00	43.45	RNA2 O
ATOM	3347	O5*	U D1078	3.288	-19.785	-50.981	1.00	30.32	RNA2 O
ATOM	3348	C5*	U D1078	1.985	-19.408	-51.478	1.00	30.56	RNA2 C
ATOM	3349	C4*	U D1078	1.896	-17.901	-51.631	1.00	32.53	RNA2 C
ATOM	3350	O4*	U D1078	2.062	-17.283	-50.329	1.00	27.97	RNA2 O
ATOM	3351	C3*	U D1078	2.967	-17.244	-52.497	1.00	36.01	RNA2 C
ATOM	3352	O3*	U D1078	2.620	-17.183	-53.871	1.00	42.75	RNA2 O
ATOM	3353	C2*	U D1078	2.990	-15.821	-51.961	1.00	36.74	RNA2 C
ATOM	3354	O2*	U D1078	1.935	-15.045	-52.493	1.00	40.26	RNA2 O
ATOM	3355	C1*	U D1078	2.744	-16.048	-50.472	1.00	35.91	RNA2 C
ATOM	3356	N1	U D1078	4.015	-16.102	-49.729	1.00	25.89	RNA2 N
ATOM	3357	C2	U D1078	4.637	-14.892	-49.423	1.00	35.33	RNA2 C
ATOM	3358	O2	U D1078	4.167	-13.800	-49.730	1.00	30.93	RNA2 O
ATOM	3359	N3	U D1078	5.830	-15.008	-48.749	1.00	28.65	RNA2 N
ATOM	3360	C4	U D1078	6.455	-16.177	-48.357	1.00	30.34	RNA2 C
ATOM	3361	O4	U D1078	7.555	-16.119	-47.795	1.00	39.15	RNA2 O
ATOM	3362	C5	U D1078	5.749	-17.376	-48.699	1.00	25.89	RNA2 C
ATOM	3363	C6	U D1078	4.584	-17.300	-49.355	1.00	28.67	RNA2 C
ATOM	3364	P	C D1079	2.674	-18.503	-54.775	1.00	37.89	RNA2 P
ATOM	3365	O1P	C D1079	2.944	-18.013	-56.153	1.00	39.80	RNA2 O
ATOM	3366	O2P	C D1079	3.558	-19.539	-54.176	1.00	37.02	RNA2 O
ATOM	3367	O5*	C D1079	1.167	-18.996	-54.704	1.00	15.08	RNA2 O

ATOM	3368	C5*	C D1079	0.145	-18.192	-55.288	1.00	23.37	RNA2 C
ATOM	3369	C4*	C D1079	-1.208	-18.608	-54.795	1.00	19.59	RNA2 C
ATOM	3370	O4*	C D1079	-1.438	-18.079	-53.467	1.00	27.26	RNA2 O
ATOM	3371	C3*	C D1079	-2.308	-17.995	-55.628	1.00	31.62	RNA2 C
ATOM	3372	O3*	C D1079	-2.525	-18.767	-56.789	1.00	35.58	RNA2 O
ATOM	3373	C2*	C D1079	-3.484	-17.941	-54.667	1.00	27.16	RNA2 C
ATOM	3374	O2*	C D1079	-4.148	-19.180	-54.551	1.00	30.55	RNA2 O
ATOM	3375	C1*	C D1079	-2.774	-17.609	-53.357	1.00	19.20	RNA2 C
ATOM	3376	N1	C D1079	-2.738	-16.155	-53.087	1.00	15.42	RNA2 N
ATOM	3377	C2	C D1079	-3.891	-15.525	-52.594	1.00	14.73	RNA2 C
ATOM	3378	O2	C D1079	-4.922	-16.196	-52.423	1.00	22.43	RNA2 O
ATOM	3379	N3	C D1079	-3.853	-14.203	-52.319	1.00	15.70	RNA2 N
ATOM	3380	C4	C D1079	-2.730	-13.512	-52.513	1.00	19.14	RNA2 C
ATOM	3381	N4	C D1079	-2.733	-12.219	-52.194	1.00	18.52	RNA2 N
ATOM	3382	C5	C D1079	-1.550	-14.119	-53.033	1.00	14.27	RNA2 C
ATOM	3383	C6	C D1079	-1.598	-15.430	-53.303	1.00	9.72	RNA2 C
ATOM	3384	P	A D1080	-2.665	-18.025	-58.200	1.00	33.84	RNA2 P
ATOM	3385	O1P	A D1080	-1.604	-16.982	-58.302	1.00	29.98	RNA2 O
ATOM	3386	O2P	A D1080	-2.762	-19.085	-59.240	1.00	51.18	RNA2 O
ATOM	3387	O5*	A D1080	-4.078	-17.315	-58.069	1.00	18.89	RNA2 O
ATOM	3388	C5*	A D1080	-5.228	-18.109	-57.802	1.00	23.14	RNA2 C
ATOM	3389	C4*	A D1080	-6.362	-17.256	-57.316	1.00	29.15	RNA2 C
ATOM	3390	O4*	A D1080	-6.077	-16.724	-55.997	1.00	31.88	RNA2 O
ATOM	3391	C3*	A D1080	-6.704	-16.028	-58.131	1.00	27.12	RNA2 C
ATOM	3392	O3*	A D1080	-7.427	-16.344	-59.312	1.00	35.45	RNA2 O
ATOM	3393	C2*	A D1080	-7.520	-15.221	-57.129	1.00	24.68	RNA2 C
ATOM	3394	O2*	A D1080	-8.839	-15.710	-57.002	1.00	23.19	RNA2 O
ATOM	3395	C1*	A D1080	-6.774	-15.502	-55.826	1.00	22.08	RNA2 C
ATOM	3396	N9	A D1080	-5.817	-14.431	-55.545	1.00	19.19	RNA2 N
ATOM	3397	C8	A D1080	-4.460	-14.391	-55.773	1.00	21.24	RNA2 C
ATOM	3398	N7	A D1080	-3.911	-13.232	-55.485	1.00	17.04	RNA2 N
ATOM	3399	C5	A D1080	-4.974	-12.465	-55.021	1.00	10.07	RNA2 C
ATOM	3400	C6	A D1080	-5.061	-11.132	-54.578	1.00	15.82	RNA2 C
ATOM	3401	N6	A D1080	-4.019	-10.295	-54.529	1.00	19.09	RNA2 N
ATOM	3402	N1	A D1080	-6.271	-10.680	-54.183	1.00	20.36	RNA2 N
ATOM	3403	C2	A D1080	-7.317	-11.517	-54.229	1.00	15.92	RNA2 C
ATOM	3404	N3	A D1080	-7.362	-12.783	-54.626	1.00	14.17	RNA2 N
ATOM	3405	C4	A D1080	-6.145	-13.200	-55.023	1.00	9.63	RNA2 C
ATOM	3406	P	U D1081	-7.413	-15.312	-60.548	1.00	31.28	RNA2 P
ATOM	3407	O1P	U D1081	-6.027	-14.791	-60.717	1.00	8.76	RNA2 O
ATOM	3408	O2P	U D1081	-8.089	-15.971	-61.696	1.00	35.73	RNA2 O
ATOM	3409	O5*	U D1081	-8.356	-14.144	-60.021	1.00	18.56	RNA2 O
ATOM	3410	C5*	U D1081	-9.643	-14.457	-59.459	1.00	22.44	RNA2 C
ATOM	3411	C4*	U D1081	-10.276	-13.222	-58.867	1.00	34.63	RNA2 C
ATOM	3412	O4*	U D1081	-9.471	-12.728	-57.771	1.00	31.00	RNA2 O











ATOM	3593	C6	G D1089	0.653	-3.505	-49.059	1.00	26.65	RNA2 C
ATOM	3594	O6	G D1089	-0.582	-3.435	-48.934	1.00	34.44	RNA2 O
ATOM	3595	N1	G D1089	1.415	-2.339	-49.098	1.00	18.23	RNA2 N
ATOM	3596	C2	G D1089	2.782	-2.292	-49.218	1.00	22.47	RNA2 C
ATOM	3597	N2	G D1089	3.341	-1.065	-49.215	1.00	23.99	RNA2 N
ATOM	3598	N3	G D1089	3.551	-3.365	-49.325	1.00	21.65	RNA2 N
ATOM	3599	C4	G D1089	2.832	-4.504	-49.293	1.00	15.76	RNA2 C
ATOM	3600	P	U D1090	9.177	-7.107	-49.459	1.00	46.88	RNA2 P
ATOM	3601	O1P	U D1090	9.375	-7.944	-48.246	1.00	47.63	RNA2 O
ATOM	3602	O2P	U D1090	9.376	-7.711	-50.800	1.00	46.50	RNA2 O
ATOM	3603	O5*	U D1090	10.098	-5.811	-49.333	1.00	47.06	RNA2 O
ATOM	3604	C5*	U D1090	11.428	-5.782	-49.876	1.00	48.58	RNA2 C
ATOM	3605	C4*	U D1090	12.040	-4.407	-49.703	1.00	55.86	RNA2 C
ATOM	3606	O4*	U D1090	11.307	-3.422	-50.482	1.00	58.42	RNA2 O
ATOM	3607	C3*	U D1090	12.027	-3.835	-48.296	1.00	57.85	RNA2 C
ATOM	3608	O3*	U D1090	13.074	-4.330	-47.488	1.00	54.72	RNA2 O
ATOM	3609	C2*	U D1090	12.152	-2.336	-48.538	1.00	56.90	RNA2 C
ATOM	3610	O2*	U D1090	13.486	-1.912	-48.750	1.00	55.53	RNA2 O
ATOM	3611	C1*	U D1090	11.345	-2.164	-49.823	1.00	47.41	RNA2 C
ATOM	3612	N1	U D1090	9.971	-1.713	-49.552	1.00	39.04	RNA2 N
ATOM	3613	C2	U D1090	9.769	-0.350	-49.369	1.00	41.49	RNA2 C
ATOM	3614	O2	U D1090	10.675	0.475	-49.415	1.00	47.92	RNA2 O
ATOM	3615	N3	U D1090	8.468	0.014	-49.123	1.00	33.29	RNA2 N
ATOM	3616	C4	U D1090	7.371	-0.820	-49.033	1.00	35.37	RNA2 C
ATOM	3617	O4	U D1090	6.255	-0.333	-48.820	1.00	43.33	RNA2 O
ATOM	3618	C5	U D1090	7.660	-2.210	-49.227	1.00	26.33	RNA2 C
ATOM	3619	C6	U D1090	8.916	-2.599	-49.476	1.00	31.79	RNA2 C
ATOM	3620	P	G D1091	12.865	-4.400	-45.899	1.00	63.03	RNA2 P
ATOM	3621	O1P	G D1091	11.489	-4.915	-45.629	1.00	48.47	RNA2 O
ATOM	3622	O2P	G D1091	14.047	-5.119	-45.346	1.00	63.48	RNA2 O
ATOM	3623	O5*	G D1091	12.909	-2.874	-45.434	1.00	53.82	RNA2 O
ATOM	3624	C5*	G D1091	14.160	-2.173	-45.369	1.00	60.37	RNA2 C
ATOM	3625	C4*	G D1091	13.939	-0.687	-45.231	1.00	57.35	RNA2 C
ATOM	3626	O4*	G D1091	13.057	-0.232	-46.291	1.00	51.52	RNA2 O
ATOM	3627	C3*	G D1091	13.275	-0.168	-43.964	1.00	64.14	RNA2 C
ATOM	3628	O3*	G D1091	14.165	-0.050	-42.851	1.00	71.95	RNA2 O
ATOM	3629	C2*	G D1091	12.766	1.197	-44.414	1.00	59.80	RNA2 C
ATOM	3630	O2*	G D1091	13.774	2.190	-44.402	1.00	67.83	RNA2 O
ATOM	3631	C1*	G D1091	12.345	0.913	-45.854	1.00	48.17	RNA2 C
ATOM	3632	N9	G D1091	10.912	0.647	-45.911	1.00	35.24	RNA2 N
ATOM	3633	C8	G D1091	10.281	-0.571	-45.991	1.00	35.20	RNA2 C
ATOM	3634	N7	G D1091	8.979	-0.474	-45.954	1.00	29.59	RNA2 N
ATOM	3635	C5	G D1091	8.739	0.890	-45.858	1.00	21.43	RNA2 C
ATOM	3636	C6	G D1091	7.518	1.604	-45.771	1.00	32.33	RNA2 C
ATOM	3637	O6	G D1091	6.364	1.159	-45.749	1.00	43.19	RNA2 O

ATOM	3638	N1	G D1091	7.731	2.976	-45.699	1.00	28.62	RNA2 N
ATOM	3639	C2	G D1091	8.961	3.582	-45.701	1.00	39.37	RNA2 C
ATOM	3640	N2	G D1091	8.965	4.920	-45.626	1.00	34.96	RNA2 N
ATOM	3641	N3	G D1091	10.107	2.925	-45.772	1.00	32.50	RNA2 N
ATOM	3642	C4	G D1091	9.920	1.594	-45.848	1.00	25.53	RNA2 C
ATOM	3643	P	C D1092	13.560	0.093	-41.358	1.00	80.57	RNA2 P
ATOM	3644	O1P	C D1092	12.499	-0.941	-41.171	1.00	72.16	RNA2 O
ATOM	3645	O2P	C D1092	14.702	0.146	-40.409	1.00	77.36	RNA2 O
ATOM	3646	O5*	C D1092	12.841	1.520	-41.356	1.00	67.00	RNA2 O
ATOM	3647	C5*	C D1092	13.608	2.728	-41.517	1.00	47.50	RNA2 C
ATOM	3648	C4*	C D1092	12.721	3.950	-41.413	1.00	46.89	RNA2 C
ATOM	3649	O4*	C D1092	11.785	3.999	-42.524	1.00	47.64	RNA2 O
ATOM	3650	C3*	C D1092	11.825	4.069	-40.193	1.00	48.58	RNA2 C
ATOM	3651	O3*	C D1092	12.485	4.523	-39.029	1.00	50.53	RNA2 O
ATOM	3652	C2*	C D1092	10.775	5.069	-40.650	1.00	46.94	RNA2 C
ATOM	3653	O2*	C D1092	11.196	6.411	-40.524	1.00	56.76	RNA2 O
ATOM	3654	C1*	C D1092	10.610	4.694	-42.122	1.00	44.37	RNA2 C
ATOM	3655	N1	C D1092	9.429	3.823	-42.282	1.00	40.91	RNA2 N
ATOM	3656	C2	C D1092	8.155	4.415	-42.217	1.00	43.01	RNA2 C
ATOM	3657	O2	C D1092	8.072	5.647	-42.083	1.00	41.14	RNA2 O
ATOM	3658	N3	C D1092	7.056	3.632	-42.298	1.00	33.92	RNA2 N
ATOM	3659	C4	C D1092	7.188	2.312	-42.444	1.00	39.14	RNA2 C
ATOM	3660	N4	C D1092	6.075	1.577	-42.496	1.00	35.85	RNA2 N
ATOM	3661	C5	C D1092	8.469	1.685	-42.538	1.00	31.59	RNA2 C
ATOM	3662	C6	C D1092	9.552	2.471	-42.458	1.00	35.03	RNA2 C
ATOM	3663	P	G D1093	11.977	4.012	-37.593	1.00	51.96	RNA2 P
ATOM	3664	O1P	G D1093	11.975	2.526	-37.626	1.00	48.41	RNA2 O
ATOM	3665	O2P	G D1093	12.764	4.724	-36.553	1.00	64.77	RNA2 O
ATOM	3666	O5*	G D1093	10.458	4.492	-37.515	1.00	35.20	RNA2 O
ATOM	3667	C5*	G D1093	10.122	5.886	-37.581	1.00	24.69	RNA2 C
ATOM	3668	C4*	G D1093	8.630	6.056	-37.704	1.00	29.37	RNA2 C
ATOM	3669	O4*	G D1093	8.164	5.435	-38.930	1.00	34.30	RNA2 O
ATOM	3670	C3*	G D1093	7.808	5.387	-36.620	1.00	33.91	RNA2 C
ATOM	3671	O3*	G D1093	7.738	6.175	-35.452	1.00	53.14	RNA2 O
ATOM	3672	C2*	G D1093	6.454	5.194	-37.289	1.00	36.57	RNA2 C
ATOM	3673	O2*	G D1093	5.628	6.344	-37.254	1.00	23.38	RNA2 O
ATOM	3674	C1*	G D1093	6.871	4.878	-38.726	1.00	33.38	RNA2 C
ATOM	3675	N9	G D1093	6.940	3.436	-38.961	1.00	31.32	RNA2 N
ATOM	3676	C8	G D1093	8.073	2.656	-39.054	1.00	27.97	RNA2 C
ATOM	3677	N7	G D1093	7.812	1.389	-39.243	1.00	30.70	RNA2 N
ATOM	3678	C5	G D1093	6.424	1.326	-39.280	1.00	27.66	RNA2 C
ATOM	3679	C6	G D1093	5.563	0.215	-39.451	1.00	30.04	RNA2 C
ATOM	3680	O6	G D1093	5.866	-0.977	-39.608	1.00	42.76	RNA2 O
ATOM	3681	N1	G D1093	4.222	0.596	-39.422	1.00	21.84	RNA2 N
ATOM	3682	C2	G D1093	3.770	1.881	-39.247	1.00	13.29	RNA2 C

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ATOM	3728	P	A	D1096	3.829	-1.151	-32.569	1.00	34.70	RNA2 P
ATOM	3729	O1P	A	D1096	4.017	0.256	-32.992	1.00	37.33	RNA2 O
ATOM	3730	O2P	A	D1096	4.838	-2.167	-32.962	1.00	24.34	RNA2 O
ATOM	3731	O5*	A	D1096	2.383	-1.617	-33.047	1.00	20.77	RNA2 O
ATOM	3732	C5*	A	D1096	1.913	-2.930	-32.724	1.00	19.81	RNA2 C
ATOM	3733	C4*	A	D1096	0.421	-3.021	-32.910	1.00	22.36	RNA2 C
ATOM	3734	O4*	A	D1096	-0.262	-2.200	-31.934	1.00	23.18	RNA2 O
ATOM	3735	C3*	A	D1096	-0.119	-2.546	-34.243	1.00	23.44	RNA2 C
ATOM	3736	O3*	A	D1096	0.028	-3.536	-35.249	1.00	37.12	RNA2 O
ATOM	3737	C2*	A	D1096	-1.575	-2.237	-33.914	1.00	26.79	RNA2 C
ATOM	3738	O2*	A	D1096	-2.392	-3.387	-33.889	1.00	29.84	RNA2 O
ATOM	3739	C1*	A	D1096	-1.458	-1.686	-32.493	1.00	23.36	RNA2 C
ATOM	3740	N9	A	D1096	-1.373	-0.228	-32.496	1.00	24.90	RNA2 N
ATOM	3741	C8	A	D1096	-0.240	0.551	-32.560	1.00	30.09	RNA2 C
ATOM	3742	N7	A	D1096	-0.485	1.838	-32.573	1.00	29.53	RNA2 N
ATOM	3743	C5	A	D1096	-1.870	1.914	-32.507	1.00	21.47	RNA2 C
ATOM	3744	C6	A	D1096	-2.751	3.005	-32.479	1.00	23.47	RNA2 C
ATOM	3745	N6	A	D1096	-2.348	4.281	-32.511	1.00	30.56	RNA2 N
ATOM	3746	N1	A	D1096	-4.075	2.741	-32.411	1.00	23.77	RNA2 N
ATOM	3747	C2	A	D1096	-4.471	1.460	-32.368	1.00	24.81	RNA2 C
ATOM	3748	N3	A	D1096	-3.736	0.349	-32.383	1.00	22.60	RNA2 N
ATOM	3749	C4	A	D1096	-2.429	0.650	-32.454	1.00	13.49	RNA2 C
ATOM	3750	P	C	D1097	0.158	-3.087	-36.781	1.00	28.43	RNA2 P
ATOM	3751	O1P	C	D1097	1.274	-2.107	-36.889	1.00	25.96	RNA2 O
ATOM	3752	O2P	C	D1097	0.208	-4.341	-37.575	1.00	39.67	RNA2 O
ATOM	3753	O5*	C	D1097	-1.234	-2.357	-37.037	1.00	17.23	RNA2 O
ATOM	3754	C5*	C	D1097	-1.317	-1.078	-37.691	1.00	20.94	RNA2 C
ATOM	3755	C4*	C	D1097	-2.742	-0.584	-37.636	1.00	29.32	RNA2 C
ATOM	3756	O4*	C	D1097	-3.029	-0.045	-36.315	1.00	40.36	RNA2 O
ATOM	3757	C3*	C	D1097	-3.106	0.550	-38.569	1.00	29.37	RNA2 C
ATOM	3758	O3*	C	D1097	-3.388	0.082	-39.870	1.00	44.58	RNA2 O
ATOM	3759	C2*	C	D1097	-4.341	1.126	-37.895	1.00	33.92	RNA2 C
ATOM	3760	O2*	C	D1097	-5.487	0.330	-38.113	1.00	32.32	RNA2 O
ATOM	3761	C1*	C	D1097	-3.945	1.037	-36.423	1.00	34.10	RNA2 C
ATOM	3762	N1	C	D1097	-3.265	2.289	-36.012	1.00	31.44	RNA2 N
ATOM	3763	C2	C	D1097	-4.047	3.417	-35.683	1.00	27.94	RNA2 C
ATOM	3764	O2	C	D1097	-5.285	3.313	-35.669	1.00	29.21	RNA2 O
ATOM	3765	N3	C	D1097	-3.427	4.588	-35.390	1.00	30.98	RNA2 N
ATOM	3766	C4	C	D1097	-2.090	4.658	-35.404	1.00	44.95	RNA2 C
ATOM	3767	N4	C	D1097	-1.519	5.838	-35.133	1.00	50.64	RNA2 N
ATOM	3768	C5	C	D1097	-1.275	3.522	-35.698	1.00	39.09	RNA2 C
ATOM	3769	C6	C	D1097	-1.897	2.370	-35.988	1.00	32.35	RNA2 C
ATOM	3770	P	A	D1098	-2.688	0.785	-41.132	1.00	43.71	RNA2 P
ATOM	3771	O1P	A	D1098	-1.216	0.563	-41.059	1.00	24.08	RNA2 O
ATOM	3772	O2P	A	D1098	-3.449	0.343	-42.334	1.00	56.53	RNA2 O

ATOM	3773	O5*	A D1098	-2.952	2.337	-40.908	1.00	42.07	RNA2 O
ATOM	3774	C5*	A D1098	-4.281	2.842	-40.702	1.00	41.90	RNA2 C
ATOM	3775	C4*	A D1098	-4.225	4.295	-40.292	1.00	49.33	RNA2 C
ATOM	3776	O4*	A D1098	-3.523	4.414	-39.025	1.00	47.73	RNA2 O
ATOM	3777	C3*	A D1098	-3.462	5.219	-41.229	1.00	50.90	RNA2 C
ATOM	3778	O3*	A D1098	-4.263	5.645	-42.324	1.00	54.47	RNA2 O
ATOM	3779	C2*	A D1098	-3.057	6.363	-40.303	1.00	47.39	RNA2 C
ATOM	3780	O2*	A D1098	-4.104	7.289	-40.085	1.00	53.57	RNA2 O
ATOM	3781	C1*	A D1098	-2.781	5.621	-38.995	1.00	36.88	RNA2 C
ATOM	3782	N9	A D1098	-1.365	5.289	-38.851	1.00	28.68	RNA2 N
ATOM	3783	C8	A D1098	-0.744	4.078	-39.051	1.00	36.76	RNA2 C
ATOM	3784	N7	A D1098	0.560	4.120	-38.906	1.00	27.01	RNA2 N
ATOM	3785	C5	A D1098	0.813	5.442	-38.575	1.00	32.11	RNA2 C
ATOM	3786	C6	A D1098	2.004	6.136	-38.311	1.00	39.08	RNA2 C
ATOM	3787	N6	A D1098	3.217	5.578	-38.364	1.00	35.79	RNA2 N
ATOM	3788	N1	A D1098	1.907	7.447	-37.996	1.00	37.08	RNA2 N
ATOM	3789	C2	A D1098	0.692	8.013	-37.969	1.00	35.02	RNA2 C
ATOM	3790	N3	A D1098	-0.498	7.470	-38.214	1.00	31.17	RNA2 N
ATOM	3791	C4	A D1098	-0.366	6.169	-38.516	1.00	35.12	RNA2 C
ATOM	3792	P	G D1099	-3.598	5.799	-43.783	1.00	57.31	RNA2 P
ATOM	3793	O1P	G D1099	-3.062	4.481	-44.215	1.00	60.32	RNA2 O
ATOM	3794	O2P	G D1099	-4.589	6.508	-44.640	1.00	60.85	RNA2 O
ATOM	3795	O5*	G D1099	-2.349	6.753	-43.537	1.00	41.11	RNA2 O
ATOM	3796	C5*	G D1099	-2.543	8.130	-43.169	1.00	50.07	RNA2 C
ATOM	3797	C4*	G D1099	-1.216	8.782	-42.888	1.00	47.05	RNA2 C
ATOM	3798	O4*	G D1099	-0.626	8.173	-41.712	1.00	46.92	RNA2 O
ATOM	3799	C3*	G D1099	-0.174	8.588	-43.975	1.00	54.47	RNA2 C
ATOM	3800	O3*	G D1099	-0.305	9.517	-45.036	1.00	55.05	RNA2 O
ATOM	3801	C2*	G D1099	1.139	8.720	-43.217	1.00	48.61	RNA2 C
ATOM	3802	O2*	G D1099	1.553	10.057	-43.029	1.00	55.32	RNA2 O
ATOM	3803	C1*	G D1099	0.781	8.073	-41.878	1.00	40.34	RNA2 C
ATOM	3804	N9	G D1099	1.140	6.659	-41.891	1.00	34.55	RNA2 N
ATOM	3805	C8	G D1099	0.293	5.577	-41.965	1.00	33.18	RNA2 C
ATOM	3806	N7	G D1099	0.926	4.437	-42.047	1.00	37.87	RNA2 N
ATOM	3807	C5	G D1099	2.270	4.787	-42.007	1.00	28.79	RNA2 C
ATOM	3808	C6	G D1099	3.437	3.978	-42.083	1.00	36.73	RNA2 C
ATOM	3809	O6	G D1099	3.519	2.747	-42.210	1.00	46.32	RNA2 O
ATOM	3810	N1	G D1099	4.596	4.744	-42.006	1.00	30.92	RNA2 N
ATOM	3811	C2	G D1099	4.630	6.113	-41.873	1.00	40.47	RNA2 C
ATOM	3812	N2	G D1099	5.847	6.678	-41.812	1.00	23.42	RNA2 N
ATOM	3813	N3	G D1099	3.549	6.876	-41.805	1.00	31.10	RNA2 N
ATOM	3814	C4	G D1099	2.415	6.152	-41.883	1.00	28.17	RNA2 C
ATOM	3815	P	C D1100	0.097	9.071	-46.522	1.00	56.56	RNA2 P
ATOM	3816	O1P	C D1100	-0.323	7.657	-46.716	1.00	63.87	RNA2 O
ATOM	3817	O2P	C D1100	-0.407	10.115	-47.447	1.00	69.36	RNA2 O

TOTAL = 5086660

ATOM	3818	O5*	C D1100	1.688	9.106	-46.507	1.00	39.12	RNA2 O
ATOM	3819	C5*	C D1100	2.380	10.337	-46.298	1.00	32.71	RNA2 C
ATOM	3820	C4*	C D1100	3.863	10.098	-46.207	1.00	40.37	RNA2 C
ATOM	3821	O4*	C D1100	4.155	9.281	-45.042	1.00	45.57	RNA2 O
ATOM	3822	C3*	C D1100	4.502	9.335	-47.356	1.00	48.34	RNA2 C
ATOM	3823	O3*	C D1100	4.774	10.136	-48.495	1.00	58.69	RNA2 O
ATOM	3824	C2*	C D1100	5.771	8.784	-46.718	1.00	42.72	RNA2 C
ATOM	3825	O2*	C D1100	6.840	9.707	-46.670	1.00	45.27	RNA2 O
ATOM	3826	C1*	C D1100	5.289	8.466	-45.303	1.00	36.28	RNA2 C
ATOM	3827	N1	C D1100	4.897	7.048	-45.234	1.00	33.17	RNA2 N
ATOM	3828	C2	C D1100	5.910	6.083	-45.177	1.00	37.72	RNA2 C
ATOM	3829	O2	C D1100	7.090	6.461	-45.104	1.00	37.78	RNA2 O
ATOM	3830	N3	C D1100	5.582	4.772	-45.201	1.00	34.10	RNA2 N
ATOM	3831	C4	C D1100	4.299	4.409	-45.268	1.00	36.21	RNA2 C
ATOM	3832	N4	C D1100	4.024	3.103	-45.330	1.00	35.52	RNA2 N
ATOM	3833	C5	C D1100	3.242	5.369	-45.283	1.00	32.04	RNA2 C
ATOM	3834	C6	C D1100	3.583	6.665	-45.263	1.00	33.05	RNA2 C
ATOM	3835	P	U D1101	4.754	9.460	-49.951	1.00	59.64	RNA2 P
ATOM	3836	O1P	U D1101	3.464	8.731	-50.077	1.00	53.79	RNA2 O
ATOM	3837	O2P	U D1101	5.117	10.490	-50.957	1.00	73.54	RNA2 O
ATOM	3838	O5*	U D1101	5.931	8.390	-49.894	1.00	44.03	RNA2 O
ATOM	3839	C5*	U D1101	7.275	8.809	-49.652	1.00	37.19	RNA2 C
ATOM	3840	C4*	U D1101	8.197	7.620	-49.625	1.00	44.44	RNA2 C
ATOM	3841	O4*	U D1101	7.844	6.748	-48.520	1.00	47.50	RNA2 O
ATOM	3842	C3*	U D1101	8.140	6.710	-50.836	1.00	49.53	RNA2 C
ATOM	3843	O3*	U D1101	8.892	7.203	-51.930	1.00	55.95	RNA2 O
ATOM	3844	C2*	U D1101	8.681	5.396	-50.286	1.00	46.03	RNA2 C
ATOM	3845	O2*	U D1101	10.091	5.371	-50.196	1.00	46.23	RNA2 O
ATOM	3846	C1*	U D1101	8.097	5.396	-48.875	1.00	41.37	RNA2 C
ATOM	3847	N1	U D1101	6.840	4.627	-48.800	1.00	33.41	RNA2 N
ATOM	3848	C2	U D1101	6.935	3.238	-48.784	1.00	34.44	RNA2 C
ATOM	3849	O2	U D1101	8.011	2.640	-48.812	1.00	33.60	RNA2 O
ATOM	3850	N3	U D1101	5.730	2.575	-48.737	1.00	17.93	RNA2 N
ATOM	3851	C4	U D1101	4.466	3.143	-48.705	1.00	36.01	RNA2 C
ATOM	3852	O4	U D1101	3.465	2.411	-48.702	1.00	25.00	RNA2 O
ATOM	3853	C5	U D1101	4.457	4.577	-48.714	1.00	24.85	RNA2 C
ATOM	3854	C6	U D1101	5.610	5.251	-48.760	1.00	26.88	RNA2 C
ATOM	3855	P	C D1102	8.485	6.763	-53.418	1.00	41.89	RNA2 P
ATOM	3856	O1P	C D1102	7.001	6.821	-53.510	1.00	43.20	RNA2 O
ATOM	3857	O2P	C D1102	9.312	7.542	-54.372	1.00	53.94	RNA2 O
ATOM	3858	O5*	C D1102	8.938	5.240	-53.483	1.00	38.14	RNA2 O
ATOM	3859	C5*	C D1102	10.317	4.889	-53.306	1.00	37.05	RNA2 C
ATOM	3860	C4*	C D1102	10.494	3.390	-53.332	1.00	45.27	RNA2 C
ATOM	3861	O4*	C D1102	9.855	2.793	-52.168	1.00	52.28	RNA2 O
ATOM	3862	C3*	C D1102	9.872	2.637	-54.498	1.00	54.50	RNA2 C

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ATOM	3863	O3*	C D1102	10.597	2.706	-55.716	1.00	57.12	RNA2 O
ATOM	3864	C2*	C D1102	9.784	1.219	-53.949	1.00	52.66	RNA2 C
ATOM	3865	O2*	C D1102	11.017	0.522	-54.000	1.00	56.57	RNA2 O
ATOM	3866	C1*	C D1102	9.401	1.482	-52.493	1.00	46.15	RNA2 C
ATOM	3867	N1	C D1102	7.932	1.399	-52.330	1.00	28.20	RNA2 N
ATOM	3868	C2	C D1102	7.331	0.128	-52.307	1.00	22.69	RNA2 C
ATOM	3869	O2	C D1102	8.053	-0.881	-52.366	1.00	35.31	RNA2 O
ATOM	3870	N3	C D1102	5.988	0.028	-52.219	1.00	9.49	RNA2 N
ATOM	3871	C4	C D1102	5.246	1.129	-52.135	1.00	16.43	RNA2 C
ATOM	3872	N4	C D1102	3.922	0.979	-52.052	1.00	15.53	RNA2 N
ATOM	3873	C5	C D1102	5.825	2.433	-52.133	1.00	15.77	RNA2 C
ATOM	3874	C6	C D1102	7.158	2.521	-52.229	1.00	21.76	RNA2 C
ATOM	3875	P	A D1103	9.806	2.525	-57.105	1.00	47.42	RNA2 P
ATOM	3876	O1P	A D1103	8.514	3.264	-57.011	1.00	38.37	RNA2 O
ATOM	3877	O2P	A D1103	10.747	2.818	-58.216	1.00	57.18	RNA2 O
ATOM	3878	O5*	A D1103	9.456	0.974	-57.138	1.00	48.19	RNA2 O
ATOM	3879	C5*	A D1103	10.493	-0.015	-56.995	1.00	51.39	RNA2 C
ATOM	3880	C4*	A D1103	9.894	-1.397	-56.965	1.00	45.50	RNA2 C
ATOM	3881	O4*	A D1103	8.978	-1.488	-55.847	1.00	45.01	RNA2 O
ATOM	3882	C3*	A D1103	9.053	-1.764	-58.178	1.00	51.96	RNA2 C
ATOM	3883	O3*	A D1103	9.867	-2.246	-59.243	1.00	53.83	RNA2 O
ATOM	3884	C2*	A D1103	8.095	-2.817	-57.622	1.00	48.46	RNA2 C
ATOM	3885	O2*	A D1103	8.635	-4.125	-57.578	1.00	47.52	RNA2 O
ATOM	3886	C1*	A D1103	7.882	-2.316	-56.192	1.00	43.28	RNA2 C
ATOM	3887	N9	A D1103	6.646	-1.549	-56.032	1.00	30.89	RNA2 N
ATOM	3888	C8	A D1103	6.477	-0.189	-55.914	1.00	25.35	RNA2 C
ATOM	3889	N7	A D1103	5.222	0.179	-55.797	1.00	26.03	RNA2 N
ATOM	3890	C5	A D1103	4.519	-1.019	-55.836	1.00	17.17	RNA2 C
ATOM	3891	C6	A D1103	3.149	-1.314	-55.759	1.00	19.87	RNA2 C
ATOM	3892	N6	A D1103	2.193	-0.387	-55.623	1.00	16.79	RNA2 N
ATOM	3893	N1	A D1103	2.784	-2.616	-55.828	1.00	26.16	RNA2 N
ATOM	3894	C2	A D1103	3.737	-3.548	-55.965	1.00	23.04	RNA2 C
ATOM	3895	N3	A D1103	5.055	-3.394	-56.049	1.00	30.58	RNA2 N
ATOM	3896	C4	A D1103	5.384	-2.090	-55.977	1.00	28.62	RNA2 C
ATOM	3897	P	C D1104	9.699	-1.627	-60.718	1.00	44.57	RNA2 P
ATOM	3898	O1P	C D1104	9.942	-0.162	-60.644	1.00	47.15	RNA2 O
ATOM	3899	O2P	C D1104	10.506	-2.463	-61.648	1.00	47.11	RNA2 O
ATOM	3900	O5*	C D1104	8.160	-1.850	-61.042	1.00	36.26	RNA2 O
ATOM	3901	C5*	C D1104	7.642	-3.172	-61.211	1.00	34.08	RNA2 C
ATOM	3902	C4*	C D1104	6.144	-3.130	-61.321	1.00	33.02	RNA2 C
ATOM	3903	O4*	C D1104	5.569	-2.739	-60.048	1.00	35.45	RNA2 O
ATOM	3904	C3*	C D1104	5.595	-2.113	-62.301	1.00	36.26	RNA2 C
ATOM	3905	O3*	C D1104	5.633	-2.561	-63.643	1.00	42.96	RNA2 O
ATOM	3906	C2*	C D1104	4.183	-1.890	-61.780	1.00	35.20	RNA2 C
ATOM	3907	O2*	C D1104	3.297	-2.916	-62.185	1.00	38.85	RNA2 O

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ATOM	3908	C1*	CD1104	4.408	-1.952	-60.268	1.00	31.46	RNA2 C
ATOM	3909	N1	CD1104	4.636	-0.606	-59.702	1.00	26.13	RNA2 N
ATOM	3910	C2	CD1104	3.528	0.178	-59.334	1.00	24.36	RNA2 C
ATOM	3911	O2	CD1104	2.386	-0.295	-59.447	1.00	21.42	RNA2 O
ATOM	3912	N3	CD1104	3.735	1.428	-58.865	1.00	27.00	RNA2 N
ATOM	3913	C4	CD1104	4.981	1.900	-58.745	1.00	31.66	RNA2 C
ATOM	3914	N4	CD1104	5.140	3.147	-58.292	1.00	37.50	RNA2 N
ATOM	3915	C5	CD1104	6.120	1.119	-59.087	1.00	19.85	RNA2 C
ATOM	3916	C6	CD1104	5.906	-0.115	-59.554	1.00	26.62	RNA2 C
ATOM	3917	P	CD1105	5.825	-1.489	-64.826	1.00	42.78	RNA2 P
ATOM	3918	O1P	CD1105	6.805	-0.460	-64.381	1.00	36.29	RNA2 O
ATOM	3919	O2P	CD1105	6.074	-2.246	-66.084	1.00	51.04	RNA2 O
ATOM	3920	O5*	CD1105	4.397	-0.802	-64.932	1.00	18.59	RNA2 O
ATOM	3921	C5*	CD1105	3.253	-1.574	-65.316	1.00	29.02	RNA2 C
ATOM	3922	C4*	CD1105	2.021	-0.711	-65.320	1.00	36.00	RNA2 C
ATOM	3923	O4*	CD1105	1.741	-0.275	-63.965	1.00	45.01	RNA2 O
ATOM	3924	C3*	CD1105	2.122	0.582	-66.111	1.00	43.97	RNA2 C
ATOM	3925	O3*	CD1105	1.919	0.405	-67.505	1.00	50.57	RNA2 O
ATOM	3926	C2*	CD1105	1.060	1.451	-65.447	1.00	42.61	RNA2 C
ATOM	3927	O2*	CD1105	-0.259	1.147	-65.873	1.00	33.02	RNA2 O
ATOM	3928	C1*	CD1105	1.225	1.048	-63.983	1.00	40.14	RNA2 C
ATOM	3929	N1	CD1105	2.173	1.938	-63.273	1.00	34.85	RNA2 N
ATOM	3930	C2	CD1105	1.704	3.161	-62.765	1.00	30.45	RNA2 C
ATOM	3931	O2	CD1105	0.516	3.473	-62.939	1.00	29.26	RNA2 O
ATOM	3932	N3	CD1105	2.558	3.975	-62.106	1.00	32.19	RNA2 N
ATOM	3933	C4	CD1105	3.836	3.622	-61.956	1.00	39.46	RNA2 C
ATOM	3934	N4	CD1105	4.644	4.466	-61.298	1.00	41.48	RNA2 N
ATOM	3935	C5	CD1105	4.346	2.391	-62.471	1.00	36.86	RNA2 C
ATOM	3936	C6	CD1105	3.488	1.587	-63.114	1.00	34.30	RNA2 C
ATOM	3937	P	AD1106	2.559	1.463	-68.538	1.00	47.42	RNA2 P
ATOM	3938	O1P	AD1106	3.960	1.743	-68.117	1.00	33.03	RNA2 O
ATOM	3939	O2P	AD1106	2.297	0.944	-69.905	1.00	51.03	RNA2 O
ATOM	3940	O5*	AD1106	1.674	2.772	-68.323	1.00	38.12	RNA2 O
ATOM	3941	C5*	AD1106	0.283	2.777	-68.706	1.00	43.96	RNA2 C
ATOM	3942	C4*	AD1106	-0.340	4.129	-68.452	1.00	51.41	RNA2 C
ATOM	3943	O4*	AD1106	-0.379	4.381	-67.026	1.00	57.25	RNA2 O
ATOM	3944	C3*	AD1106	0.391	5.331	-69.029	1.00	56.31	RNA2 C
ATOM	3945	O3*	AD1106	0.086	5.559	-70.396	1.00	55.12	RNA2 O
ATOM	3946	C2*	AD1106	-0.076	6.467	-68.126	1.00	56.95	RNA2 C
ATOM	3947	O2*	AD1106	-1.351	6.970	-68.478	1.00	57.32	RNA2 O
ATOM	3948	C1*	AD1106	-0.169	5.761	-66.776	1.00	49.81	RNA2 C
ATOM	3949	N9	AD1106	1.065	5.896	-66.003	1.00	39.90	RNA2 N
ATOM	3950	C8	AD1106	2.098	4.994	-65.902	1.00	41.00	RNA2 C
ATOM	3951	N7	AD1106	3.070	5.388	-65.116	1.00	41.71	RNA2 N
ATOM	3952	C5	AD1106	2.652	6.635	-64.672	1.00	37.31	RNA2 C

ATOM	3953	C6	A D1106	3.238	7.572	-63.805	1.00	36.44	RNA2 C
ATOM	3954	N6	A D1106	4.419	7.389	-63.208	1.00	40.12	RNA2 N
ATOM	3955	N1	A D1106	2.563	8.720	-63.570	1.00	38.29	RNA2 N
ATOM	3956	C2	A D1106	1.380	8.904	-64.178	1.00	37.00	RNA2 C
ATOM	3957	N3	A D1106	0.726	8.097	-65.014	1.00	37.07	RNA2 N
ATOM	3958	C4	A D1106	1.423	6.965	-65.219	1.00	37.01	RNA2 C
ATOM	3959	P	G D1107	1.186	6.251	-71.341	1.00	60.89	RNA2 P
ATOM	3960	O1P	G D1107	2.513	5.650	-71.037	1.00	51.64	RNA2 O
ATOM	3961	O2P	G D1107	0.665	6.218	-72.732	1.00	66.72	RNA2 O
ATOM	3962	O5*	G D1107	1.226	7.763	-70.838	1.00	59.43	RNA2 O
ATOM	3963	C5*	G D1107	0.098	8.639	-71.043	1.00	70.93	RNA2 C
ATOM	3964	C4*	G D1107	0.341	9.984	-70.392	1.00	70.62	RNA2 C
ATOM	3965	O4*	G D1107	0.347	9.841	-68.945	1.00	70.80	RNA2 O
ATOM	3966	C3*	G D1107	1.673	10.648	-70.701	1.00	69.85	RNA2 C
ATOM	3967	O3*	G D1107	1.703	11.337	-71.937	1.00	68.76	RNA2 O
ATOM	3968	C2*	G D1107	1.852	11.589	-69.519	1.00	71.85	RNA2 C
ATOM	3969	O2*	G D1107	1.134	12.799	-69.666	1.00	74.63	RNA2 O
ATOM	3970	C1*	G D1107	1.278	10.751	-68.377	1.00	66.31	RNA2 C
ATOM	3971	N9	G D1107	2.356	9.990	-67.753	1.00	61.03	RNA2 N
ATOM	3972	C8	G D1107	2.765	8.710	-68.056	1.00	64.56	RNA2 C
ATOM	3973	N7	G D1107	3.811	8.330	-67.371	1.00	62.08	RNA2 N
ATOM	3974	C5	G D1107	4.100	9.417	-66.555	1.00	59.12	RNA2 C
ATOM	3975	C6	G D1107	5.134	9.600	-65.598	1.00	54.80	RNA2 C
ATOM	3976	O6	G D1107	6.035	8.812	-65.270	1.00	51.34	RNA2 O
ATOM	3977	N1	G D1107	5.056	10.854	-65.001	1.00	50.79	RNA2 N
ATOM	3978	C2	G D1107	4.109	11.810	-65.287	1.00	54.33	RNA2 C
ATOM	3979	N2	G D1107	4.199	12.959	-64.606	1.00	51.64	RNA2 N
ATOM	3980	N3	G D1107	3.146	11.653	-66.176	1.00	49.03	RNA2 N
ATOM	3981	C4	G D1107	3.201	10.443	-66.769	1.00	58.09	RNA2 C
ATOM	3982	P	C D1108	3.118	11.599	-72.654	1.00	71.56	RNA2 P
ATOM	3983	O1P	C D1108	3.923	10.353	-72.579	1.00	60.79	RNA2 O
ATOM	3984	O2P	C D1108	2.828	12.209	-73.977	1.00	78.78	RNA2 O
ATOM	3985	O5*	C D1108	3.837	12.677	-71.723	1.00	69.28	RNA2 O
ATOM	3986	C5*	C D1108	3.274	13.992	-71.536	1.00	65.61	RNA2 C
ATOM	3987	C4*	C D1108	4.139	14.809	-70.605	1.00	60.04	RNA2 C
ATOM	3988	O4*	C D1108	4.193	14.171	-69.304	1.00	61.74	RNA2 O
ATOM	3989	C3*	C D1108	5.598	14.965	-71.001	1.00	60.53	RNA2 C
ATOM	3990	O3*	C D1108	5.901	15.783	-72.134	1.00	66.71	RNA2 O
ATOM	3991	C2*	C D1108	6.282	15.272	-69.677	1.00	63.96	RNA2 C
ATOM	3992	O2*	C D1108	6.155	16.631	-69.306	1.00	69.72	RNA2 O
ATOM	3993	C1*	C D1108	5.457	14.420	-68.706	1.00	64.54	RNA2 C
ATOM	3994	N1	C D1108	6.098	13.130	-68.372	1.00	61.20	RNA2 N
ATOM	3995	C2	C D1108	7.127	13.116	-67.417	1.00	59.89	RNA2 C
ATOM	3996	O2	C D1108	7.454	14.179	-66.867	1.00	54.39	RNA2 O
ATOM	3997	N3	C D1108	7.739	11.946	-67.119	1.00	60.31	RNA2 N

ATOM	3998	C4	C	D1108	7.359	10.821	-67.728	1.00	62.68	RNA2 C
ATOM	3999	N4	C	D1108	7.999	9.689	-67.411	1.00	63.03	RNA2 N
ATOM	4000	C5	C	D1108	6.308	10.803	-68.693	1.00	64.65	RNA2 C
ATOM	4001	C6	C	D1108	5.711	11.968	-68.982	1.00	64.25	RNA2 C
TER	4002		C	D1108						
HETATM	4003	CD	CD	201	4.250	-2.291	-5.735	0.91	77.47	CD
HETATM	4004	CD	CD	202	5.716	1.827	1.431	0.91	32.35	CD
HETATM	4005	O	HOH	205	7.540	-4.792	-0.436	1.00	19.29	O
HETATM	4006	O	HOH	209	8.097	9.026	-9.315	1.00	27.99	O
HETATM	4007	MG	MG	210	7.174	1.073	-14.750	1.00	31.99	MG
HETATM	4008	CD	CD	211	3.380	6.488	-27.905	0.91	47.98	CD
HETATM	4009	O	HOH	213	-0.304	4.175	-0.867	1.00	38.63	O
HETATM	4010	MG	MG	214	-17.505	21.323	11.148	1.00	36.28	MG
HETATM	4011	MG	MG	215	-1.702	7.910	-11.196	1.00	23.07	MG
HETATM	4012	O	HOH	216	-3.510	9.209	-16.056	1.00	43.93	O
HETATM	4013	O	HOH	217	-4.416	-0.858	-2.563	1.00	53.29	O
HETATM	4014	O	HOH	218	6.288	-5.327	-3.385	1.00	23.44	O
HETATM	4015	O	HOH	221	-1.778	1.682	-3.132	1.00	35.80	O
HETATM	4016	O	HOH	222	-6.849	10.117	-5.442	1.00	24.81	O
HETATM	4017	MG	MG	223	14.749	-5.902	12.250	1.00	36.97	MG
HETATM	4018	MG	MG	225	19.765	-8.266	10.030	1.00	41.29	MG
HETATM	4019	MG	MG	226	4.983	5.583	-14.224	1.00	17.24	MG
HETATM	4020	HG	HG	227	10.163	10.934	-4.731	0.10	21.14	HG
HETATM	4021	MG	MG	228	0.368	-4.197	15.065	1.00	49.67	MG
HETATM	4022	HG	HG	230	-4.955	2.266	-15.287	0.41	65.01	HG
HETATM	4023	O	HOH	232	17.184	-8.123	12.078	1.00	46.90	O
HETATM	4024	O	HOH	233	5.132	-9.156	11.493	1.00	39.77	O
HETATM	4025	O	HOH	235	-2.182	2.520	-0.424	1.00	32.75	O
HETATM	4026	O	HOH	236	3.337	3.950	-2.832	1.00	22.74	O
HETATM	4027	O	HOH	237	-0.294	3.992	-4.949	1.00	41.19	O
HETATM	4028	O	HOH	238	3.987	7.706	-7.271	1.00	22.33	O
HETATM	4029	O	HOH	239	-2.682	1.061	-25.220	1.00	28.52	O
HETATM	4030	O	HOH	241	-0.901	-1.716	11.637	1.00	34.24	O
HETATM	4031	O	HOH	243	13.905	-12.456	1.182	1.00	61.18	O
HETATM	4032	O	HOH	244	-6.595	6.151	4.226	1.00	33.67	O
HETATM	4033	O	HOH	245	-10.614	11.084	18.691	1.00	47.29	O
HETATM	4034	O	HOH	246	2.153	6.645	-5.263	1.00	42.17	O
HETATM	4035	O	HOH	254	1.596	7.517	-28.596	1.00	20.43	O
HETATM	4036	O	HOH	255	5.496	5.982	-27.129	1.00	15.56	O
HETATM	4037	O	HOH	256	5.082	7.342	-29.082	1.00	15.30	O
HETATM	4038	MG	MG	257	4.272	8.284	-11.053	1.00	18.63	MG
HETATM	4039	O	HOH	258	5.759	9.095	-9.332	1.00	22.95	

HETATM	4043	O	HOH	262	2.003	-1.889	-6.293	1.00	39.08	O
HETATM	4044	O	HOH	263	6.523	-2.887	-3.470	1.00	31.47	O
HETATM	4045	O	HOH	264	5.691	-4.152	-6.413	1.00	49.36	O
HETATM	4046	O	HOH	265	13.164	-1.037	-13.541	1.00	53.81	O
HETATM	4047	O	HOH	266	1.658	-4.440	-6.534	1.00	54.55	O
HETATM	4048	O	HOH	267	4.147	-0.985	-10.097	1.00	21.21	O
HETATM	4049	O	HOH	268	7.729	0.998	-17.041	1.00	32.76	O
HETATM	4050	O	HOH	269	9.473	0.412	-15.439	1.00	22.86	O
HETATM	4051	O	HOH	270	5.281	1.436	-15.928	1.00	30.01	O
HETATM	4052	O	HOH	271	5.086	-1.392	-12.878	1.00	29.98	O
HETATM	4053	O	HOH	272	5.284	18.973	-15.526	1.00	29.56	O
HETATM	4054	MG	MG	273	5.268	8.632	9.371	1.00	35.80	MG
HETATM	4055	O	HOH	274	4.009	8.265	7.258	1.00	21.81	O
HETATM	4056	O	HOH	275	6.536	8.905	7.475	1.00	34.86	O
HETATM	4057	O	HOH	276	3.058	8.060	9.657	1.00	31.13	O
HETATM	4058	O	HOH	277	5.081	6.362	8.463	1.00	31.02	O
HETATM	4059	O	HOH	278	3.600	10.499	8.517	1.00	50.03	O
HETATM	4060	CD	CD	302	0.011	-4.071	-53.380	0.91	31.52	CD
HETATM	4061	O	HOH	305	1.845	2.702	-51.597	1.00	14.19	O
HETATM	4062	CD	CD	311	4.100	-9.327	-24.111	0.91	76.29	CD
HETATM	4063	O	HOH	313	-1.010	-7.500	-47.833	1.00	40.72	O
HETATM	4064	MG	MG	318	1.219	3.097	-48.942	1.00	17.48	MG
HETATM	4065	O	HOH	322	-10.157	-13.890	-44.431	1.00	41.81	O
HETATM	4066	MG	MG	326	2.778	-7.878	-38.005	1.00	11.66	MG
HETATM	4067	O	HOH	327	9.652	-2.170	-38.994	1.00	44.35	O
HETATM	4068	HG	HG	332	-7.089	-5.545	-35.006	0.60	82.38	HG
HETATM	4069	O	HOH	333	1.493	-12.458	-57.479	1.00	39.19	O
HETATM	4070	O	HOH	335	-4.211	7.242	-62.792	1.00	49.93	O
HETATM	4071	O	HOH	336	-7.759	-5.212	-49.585	1.00	35.75	O
HETATM	4072	O	HOH	338	-3.953	-6.679	-45.543	1.00	38.41	O
HETATM	4073	O	HOH	339	0.508	-10.010	-44.801	1.00	28.38	O
HETATM	4074	O	HOH	340	-8.610	1.401	-65.472	1.00	31.42	O
HETATM	4075	O	HOH	343	5.058	-10.891	-43.391	1.00	29.07	O
HETATM	4076	O	HOH	345	5.817	-19.070	-33.612	1.00	35.77	O
HETATM	4077	O	HOH	346	8.758	-14.281	-46.244	1.00	40.41	O
HETATM	4078	HG	HG	347	6.715	-12.669	-48.448	0.20	54.24	HG
HETATM	4079	O	HOH	349	5.113	-13.530	-54.095	1.00	42.05	O
HETATM	4080	O	HOH	352	6.195	-6.263	-57.438	1.00	39.69	O
HETATM	4081	O	HOH	353	12.125	3.149	-49.649	1.00	38.23	O
HETATM	4082	MG	MG	354	11.145	8.122	-61.981	1.00	29.67	MG
HETATM	4083	O	HOH	355	10.792	7.517	-64.576	1.00	68.09	O
HETATM	4084	O	HOH	356	12.630	7.721	-60.264	1.00	42.56	O



HETATM 4133 O HOH 410 -6.651 -19.456 -54.939 1.00 26.78 O  
 HETATM 4134 O HOH 411 -2.899 -18.491 -49.891 1.00 31.34 O  
 HETATM 4135 O HOH 412 -4.041 -25.738 -47.368 1.00 61.51 O  
 HETATM 4136 CD CD 413 -13.027 8.492 10.933 0.10 33.43 CD  
 HETATM 4137 CD CD 414 -11.592 5.003 -2.412 0.10 14.13 CD  
 HETATM 4138 HG HG 415 -23.456 -2.491 -20.626 0.10 35.19 HG  
 HETATM 4139 HG HG 416 -17.183 -2.624 -19.816 0.10 45.02 HG  
 HETATM 4140 O HOH 418 -0.113 29.557 -9.189 1.00 36.18 O  
 HETATM 4141 O HOH 419 -1.958 16.568 4.135 1.00 22.82 O  
 HETATM 4142 O HOH 420 0.874 15.995 -1.216 1.00 36.22 O  
 HETATM 4143 O HOH 421 -0.098 21.800 -5.101 1.00 35.12 O  
 HETATM 4144 O HOH 422 -1.412 23.130 -2.906 1.00 36.67 O  
 HETATM 4145 O HOH 423 -3.317 24.792 0.592 1.00 45.31 O  
 HETATM 4146 O HOH 424 0.019 9.295 -10.598 1.00 36.37 O  
 HETATM 4147 O HOH 425 -2.568 8.364 -13.958 1.00 50.92 O  
 HETATM 4148 O HOH 426 -2.689 18.373 -24.066 1.00 34.21 O  
 HETATM 4149 O HOH 427 7.170 6.156 -29.910 1.00 17.29 O  
 HETATM 4150 O HOH 428 8.929 4.171 -22.749 1.00 41.67 O  
 HETATM 4151 O HOH 429 12.036 0.863 -14.965 1.00 42.52 O  
 HETATM 4152 O HOH 431 -1.202 8.279 12.504 1.00 41.33 O  
 HETATM 4153 O HOH 432 8.485 7.265 7.104 1.00 46.57 O  
 HETATM 4154 O HOH 434 4.018 10.172 4.758 1.00 37.32 O  
 HETATM 4155 O HOH 435 18.225 -9.006 -2.120 1.00 60.80 O  
 HETATM 4156 MG MG 437 11.760 -10.915 4.311 1.00 47.79 MG  
 HETATM 4157 O HOH 438 12.113 -10.561 1.951 1.00 58.11 O  
 HETATM 4158 O HOH 440 14.043 -10.435 3.845 1.00 43.62 O  
 HETATM 4159 O HOH 441 9.524 -10.398 4.381 1.00 41.20 O  
 HETATM 4160 O HOH 442 11.946 -13.321 4.538 1.00 65.98 O  
 HETATM 4161 O HOH 443 12.227 -8.461 4.164 1.00 61.70 O  
 HETATM 4162 O HOH 444 1.040 4.817 -2.689 1.00 32.93 O  
 HETATM 4163 O HOH 445 4.226 0.914 2.202 1.00 3.57 O  
 HETATM 4164 O HOH 446 6.340 -0.071 1.151 1.00 19.50 O  
 HETATM 4165 O HOH 447 4.234 3.232 1.596 1.00 12.18 O  
 HETATM 4166 HG HG 448 -4.015 -8.066 -15.150 0.10 21.04 HG  
 HETATM 4167 O HOH 450 -4.907 -3.163 -52.117 1.00 24.48 O  
 HETATM 4168 HG HG 451 -5.485 5.932 -35.358 0.10 26.20 HG  
 HETATM 4169 O HOH 452 -4.427 1.650 -44.668 1.00 47.88 O  
 HETATM 4170 O HOH 453 -6.126 -4.197 -47.630 1.00 40.28 O  
 HETATM 4171 O HOH 454 -14.902 -5.184 -53.399 1.00 41.04 O  
 HETATM 4172 O HOH 455 2.198 -31.615 -45.895 1.00 38.45 O  
 HETATM 4173 O HOH 456 -0.111 -29.053 -48.914 1.00 37.64 O  
 HETATM 4174 O HOH 457 5.023 -28.677 -39.390 1.00 42.30 O  
 HETATM 4175 O HOH 459 -8.700 -0.565 -36.045 1.00 32.85 O  
 HETATM 4176 O HOH 460 -1.593 -4.423 -51.572 1.00 28.40 O  
 HETATM 4177 O HOH 461 -1.729 -3.181 -53.813 1.00 2.00 O

